STIC Search Report
Biotech-Chem Library

TO: Sumesh Kaushal
Location: REM-2B85&2C70
Art Unit: 1633
Monday, August 08, 2005

Case Serial Number: 10/787382

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: August 4, 2005, 17:01:52 ; Search time 33.9036 Seconds
                 (without alignments)
                 295.042 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLLNLSLLALGAAYVSAF.........FLDYLQVFLGVINTEWTPES 134

Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
                 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   Issued Patents AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	696	100.0	134	4	US-09-322-409-81	Sequence 81, Appl
2	696	100.0	134	4	US-09-451-527-81	Sequence 81, Appl
3	687	98.7	134	4	US-09-371-615A-2	Sequence 2, Appl
4	610	87.6	115	4	US-09-322-409-86	Sequence 86, Appl
5	610	87.6	115	4	US-09-451-527-86	Sequence 86, Appl
6	430	61.8	134	1	US-08-284-393B-13	Sequence 13, Appl
7	430	61.8	134	3	US-09-371-615A-7	Sequence 7, Appl
8	430	61.8	134	4	US-08-759-628-9	Sequence 9, Appl
9	430	61.8	134	4	US-09-371-615A-7	Sequence 7, Appl
10	430	61.8	134	5	PCT-US95-08950-13	Sequence 13, Appl
11	430	61.8	134	6	5324640-2	Sequence 2, Appl
12	430	61.8	133	4	US-09-556-818-1	Sequence 1, Appli
13	376	54.0	115	4	US-09-371-615A-8	Sequence 8, Appli
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16	339	48.7	126	4	US-09-556-818-6	Sequence 6, Appli
17	335	48.1	132	4	US-09-451-527-86	Sequence 86, Appl
18	332.5	47.8	126	4	US-09-556-818-2	Sequence 2, Appl
19	332.5	47.8	126	4	US-09-556-818-28	Sequence 28, Appl
20	331.5	47.6	132	4	US-09-556-818-40	Sequence 40, Appl
21	330.5	47.5	124	4	US-09-556-818-34	Sequence 34, Appl
22	330.5	47.5	132	4	US-09-556-818-9	Sequence 9, Appl
23	329.5	47.3	132	4	US-09-556-818-7	Sequence 7, Appli
24	328.5	47.2	130	4	US-09-556-818-32	Sequence 32, Appli
25	328.5	47.2	130	4	US-09-556-818-44	Sequence 44, Appl
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28	321.5	46.2	124	4	US-09-556-818-5	Sequence 5, Appli
29	321	46.2	124	4	US-09-556-818-38	Sequence 38, Appl
30	321	46.1	124	4	US-09-556-818-17	Sequence 17, Appl
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33	317	45.5	113	4	US-09-556-818-60	Sequence 60, Appl
34	317	45.5	130	4	US-09-556-818-50	Sequence 50, Appl
35	315.5	45.3	128	4	US-09-556-818-21	Sequence 21, Appl
36	311	44.7	145	4	US-09-556-818-60	Sequence 60, Appl
37	309.5	44.5	122	4	US-09-556-818-58	Sequence 58, Appl
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39	301.5	43.3	118	4	US-09-556-818-3	Sequence 3, Appli
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43	299.5	43.0	124	4	US-09-556-818-30	Sequence 30, Appl
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47	289.5	41.6	116	4	US-09-556-818-52	Sequence 52, Appl
48	289.5	41.6	128	4	US-09-556-818-20	Sequence 20, Appl
49	287.5	41.3	122	4	US-09-556-818-48	Sequence 48, Appl
50	282.5	40.6	122	4	US-09-556-818-22	Sequence 22, Appl
51	282.5	40.6	139	4	US-09-556-818-14	Sequence 14, Appl
52	263.5	37.9	116	4	US-09-556-818-19	Sequence 19, Appl
53	261.5	37.6	122	4	US-09-556-818-62	Sequence 62, Appli
54	75	10.8	19	4	US-09-489-847-280	Sequence 280, App
55	74	10.7	323	4	US-09-134-000C-5535	Sequence 5535, App
56	72.5	10.4	686	4	US-09-914-259-33	Sequence 33, Appl
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58	71.5	10.3	521	4	US-09-248-796A-14631	Sequence 14631, A
59	71.5	10.3	599	4	US-09-543-681A-6857	Sequence 6857, Appl
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69	69.5	10.0	1187	3	US-08-664-962B-8	Sequence 8, Appli
70	69.5	10.0	1187	3	US-09-311-743-8	Sequence 8, Appli
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72	69.5	10.0	1189	3	US-09-195-868-15	Sequence 15, Appl
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74	68.5	9.8	517	4	US-09-248-796A-21314	Sequence 21314, A
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77	68	9.8	406	4	US-09-902-540-13016	Sequence 13016, A
78	67.5	9.7	254	4	US-09-809-665A-10	Sequence 10, Appl
79	67.5	9.7	364	1	US-09-252-991A-18473	Sequence 18473, A
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83	67	9.6	2311	3	US-08-934-386-9	Sequence 9, Appli
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99	66	9.5	2325	4	US-08-695-651-6	Sequence 6, Appli
100	66	9.5	2325	3	US-08-930-285-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-322-409-81
; Sequence 81, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09,322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-81

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Best Local Similarity 100.0%; Pred. No. 5e-81;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 VFLGVINTEWTPES 134
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Db 121 VFLGVINTEWTPES 134

RESULT 2
US-09-451-527-81
; Sequence 81, Application US/09451527
; Patent No. 648243
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-81

Query Match 100.0%; Score 696; DB 4; Length 134;

Best Local Similarity 100.0%; Pred. No. 5e-81; Mismatches 0;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 VFLGVINTEWTPES 134
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RESULT 3
US-09-371-615A-2
; Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 0360400170OUSOO
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-371-615A-2

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Best Local Similarity 99.3%; Pred. No. 7.1e-80;
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 VFLGVINTEWTPES 134
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Db 121 VFLGVINTEWTPES 134

RESULT 4
US-09-322-409-86
; Sequence 86, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT

; ORGANISM: Canis familiaris
US-09-322-409-86

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Best Local Similarity   87.6%;   Score 610;   Pred. No. 4.1e-70;   Length 115;
Matches 115;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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RESULT 5
US-09-451-527-86
; Sequence 86, Application US/09451527
; Patent No. 648203
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Dreitz, Matthew J.
;   APPLICANT: Wonderling, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C2
;   CURRENT APPLICATION NUMBER: US/09/451,527
;   CURRENT FILING DATE: 1999-12-01
;   EARLIER APPLICATION NUMBER: 09/322,409
;   EARLIER FILING DATE: 1999-05-28
;   EARLIER APPLICATION NUMBER: 60/087,306
;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 86
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-451-527-86

Query Match
Best Local Similarity   87.6%;   Score 610;   DB 4;   Length 115;
Matches 115;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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RESULT 6
US-08-284-393B-13
; Sequence 13, Application US/08284393B
; Patent No. 569234
; GENERAL INFORMATION:
;   APPLICANT: Zurawski, Sandra M.
;   APPLICANT: Zurawski, Gerard
;   TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: DNAX Research Institute
;   STREET: 901 California Avenue
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/284,393B
;   FILING DATE: 01-AUG-1994
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ching, Edwin P.
;   REGISTRATION NUMBER: 34,090
;   REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-852-9196
;   TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 134 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-284-393B-13

Query Match
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Matches 87;   Conservative 17;   Mismatches 30;   Indels 0;   Gaps 0;

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Qy   61  QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
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RESULT 7
US-08-759-628-9
; Sequence 9, Application US/08759628
; Patent No. 6225446
; GENERAL INFORMATION:
;   APPLICANT: Altmann, Scott W.
;   APPLICANT: Rock, Fernando L.
;   APPLICANT: Bazan, J. Fernando
;   APPLICANT: Kastelein, Robert A.
;   TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: DNAX Research Institute
;   STREET: 901 California Avenue
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/759,628
;   FILING DATE: 05-DEC-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/008,574
;   FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ching, Edwin P.
;   REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0552Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 20..134
; OTHER INFORMATION: /note= "peptide of Figure 1"
US-08-759-628-9

Qy   1 MRMLLNLSILALGAAYVSAFAVENPMNRLVAEFITLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRMLLHLSILALGAAYVSAFAVENPMNRLVAEFITLTLLSTHRTWLIGDGNLMIPTPENKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
          | ||||:|||||||||||||||||||:|:||:||||||||||||:||||||||| ||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
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Db   121 EFLGVMNTEWIIES 134

RESULT 8
US-09-371-615A-7
; Sequence 7, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 036040017000US0
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Interleukin 5
US-09-371-615A-7

Query Match   61.8%;   Score 430;   DB 4;   Length 134;
Best Local Similarity   64.9%;   Pred. No. 5.8e-47;
Matches   87;   Conservative   17;   Mismatches   30;   Indels   0;   Gaps   0;

Qy   1 MRMLLNLSILALGAAYVSAFAVENPMNRLVAEFITLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRMLLHLSILALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
          | ||||:|||||||||||||||||||:|:||:||||||||||||:||||||||| ||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
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Db   121 EFLGVMNTEWIIES 134

US-09-462-941-12
; Sequence 12, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-12

Query Match   61.8%;   Score 430;   DB 4;   Length 134;
Best Local Similarity   64.9%;   Pred. No. 5.8e-47;
Matches   87;   Conservative   17;   Mismatches   30;   Indels   0;   Gaps   0;

Qy   1 MRMLLNLSILALGAAYVSAFAVENPMNRLVAEFITLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRMLLHLSILALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
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Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
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Db   121 EFLGVMNTEWIIES 134

RESULT 10
PCT-US95-08950-13
; Sequence 13, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

RESULT 9

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;       LENGTH: 134 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
PCT-US95-08950-13

Query Match        61.8%;  Score 430;  DB 5;  Length 134;
Best Local Similarity   64.9%;  Pred. No. 5.8e-47;
Matches   87;  Conservative  17;  Mismatches  30;  Indels  0;  Gaps  0;

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Db     1  MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH  60

Qy    61  QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
Db    61  QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy   121  VFLGVINTEWTPES 134
Db   121  EFLGVMNTEWIIES 134


RESULT 11
5324640-2
;Patent No. 5324640
;       APPLICANT: Honjo, Tasuku;Takatsu, Kiyoshi;Severinson, Eva
;       TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
;PROCESS OF PRODUCING SAID FACTOR
;       NUMBER OF SEQUENCES: 2
;       CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE: 21-SEP-1987
;SEQ ID NO:2:
;       LENGTH: 134.
5324640-2


RESULT 12
5324640-2
;Patent No. 5324640
;       APPLICANT: Honjo, Tasuku;Takatsu, Kiyoshi;Severinson, Eva
;       TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
;PROCESS OF PRODUCING SAID FACTOR
;       NUMBER OF SEQUENCES: 2
;       CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/07/99,467
;       FILING DATE: 21-SEP-1987
;SEQ ID NO:2:
;       LENGTH: 134

Query Match        61.8%;  Score 430;  DB 6;  Length 134;
Best Local Similarity   64.9%;  Pred. No. 5.8e-47;
Matches   87;  Conservative  17;  Mismatches  30;  Indels  0;  Gaps  0;

Qy     1  MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH  60
Db     1  MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH  60

Qy    61  QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
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Qy   121  VFLGVINTEWTPES 134
Db   121  EFLGVMNTEWIIES 134


RESULT 13
US-09-371-615A-8
;Sequence 8, Application US/09371615A
;Patent No. 6537781
;GENERAL INFORMATION:
;       APPLICANT: IDEXX LABORATORIES
;       TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
;       TITLE OF INVENTION: CANINE INTERLEUKIN 5
;       FILE REFERENCE: 03604001700US00
;       CURRENT APPLICATION NUMBER: US/09/371,615A
;       CURRENT FILING DATE: 1999-08-10
;       NUMBER OF SEQ ID NOS: 8
;       SOFTWARE: FastSEQ for Windows Version 3.0
;SEQ ID NO 8
;       LENGTH: 133
;       TYPE: PRT
;       ORGANISM: Mus musculus
;       FEATURE:
;       OTHER INFORMATION: Interleukin 5
US-09-371-615A-8

Query Match        54.0%;  Score 376;  DB 4;  Length 133;
Best Local Similarity   56.8%;  Pred. No. 4.7e-40;
Matches   75;  Conservative  21;  Mismatches  34;  Indels  2;  Gaps  1;

Qy     2  RMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQ  61
Db     3  RMLLHLSVLTLSCVW--ATAMBIPMSTVVKETLTQLSAHRALLTSNETMRLPVPVTKNHQ  60

Qy    62  LCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQV 121
Db    61  LCIGEIFQGIDILKNQTVRGGTVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQE 120

Qy   122  FLGVINTEWTPES 133
Db   121  FLGVMSTEWAME  132


RESULT 14
US-09-556-818-1
;Sequence 1, Application US/09556818
;Patent No. 6746669
;GENERAL INFORMATION:
;       APPLICANT: Klysner, Steen
;       TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
;       FILE REFERENCE: 0459-0428P
;       CURRENT APPLICATION NUMBER: US/09/556,818
;       CURRENT FILING DATE: 2000-04-21
;       NUMBER OF SEQ ID NOS: 65
;       SOFTWARE: PatentIn Ver. 2.1
;SEQ ID NO 1
;       LENGTH: 115
;       TYPE: PRT
;       ORGANISM: Homo sapiens
;       FEATURE:
;       NAME/KEY: DISULFID
;       LOCATION: (44)
;       OTHER INFORMATION: DISULFID
;       OTHER INFORMATION: Interchain disulphide bond to Cys-86 in SEQ ID
;       NAME/KEY: DISULFID
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;   LOCATION: (86)
;   OTHER INFORMATION: Interchain disulphide bond to Cys-44 in SEQ ID
;   OTHER INFORMATION: NO:1
US-09-556-818-1

Query Match             51.1%;   Score 356;   DB 4;   Length 115;
Best Local Similarity   62.5%;   Pred. No. 1.4e-37;
Matches 70;   Conservative 16;   Mismatches 26;   Indels 0;   Gaps 0;

Qy    23  ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE  82
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Db     4  EIPTSALVKRTLALLSTHRTLLIANETLRIPVPVHKNHQLCTERIFQGIGTLRSQTVQGG  63

Qy    83  AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES  134
              |:||:|||||||||::||:||||||| |:|||||||| |||||||  |
Db    64  TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYLQEFLGVWNTEWIIES  115
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RESULT 15
US-09-180-864-2
;   Sequence 2, Application US/09180864
;   Patent No. 6465616
;   GENERAL INFORMATION:
;   APPLICANT: Lopez, Angel
;   APPLICANT: Vadas, Matthew
;   APPLICANT: Shannon, Frances
;   APPLICANT: Bastiras, Stan
;   APPLICANT: Hey, Allan W
;   TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
;   FILE REFERENCE: 9972Z
;   CURRENT APPLICATION NUMBER: US/09/180,864
;   CURRENT FILING DATE: 1999-04-12
;   PRIOR APPLICATION NUMBER: 08/591,438
;   PRIOR FILING DATE: 1994-07-28
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 2
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: modified IL-5
US-09-180-864-2

Query Match   50.4%;   Score 351;   DB 4;   Length 121;
Best Local Similarity   61.6%;   Pred. No. 6.5e-37;
Matches 69;   Conservative 16;   Mismatches 27;   Indels 0;   Gaps 0;

Qy   23 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 82
              :|| ||||||||||||||||| :| |: :|||||||| ||:||||| |||:|||—|
Db   10 EIPTSALVKRTLALLSTHRTLLIANETLRIPVPVHKNHQLCTERIFQGIGTLRSQTVQGG 69

Qy   83 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
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Db   70 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYLQEFLGVWNTEWIIES 121
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Search completed: August 4, 2005, 17:13:06
Job time : 35.9036 secs
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 6, 2005, 19:38:05 ; Search time 2459.9 Seconds
(without alignments)
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Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLLNLSLLALGAAYVSAF.........FLDYLQVFLGVINTEWTPES 134

Scoring table: BLOSUM62

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7

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3: gb_in:*
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9: gb_pr:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	696	100.0	402	6	BD211560	BD211560 Canine an
c 5	696	100.0	402	6	AR254494	AR254494 Sequence
c 6	696	100.0	402	6	AR254495	AR254495 Sequence
c 7	696	100.0	402	4	AF331919	AF331919 Canis fam
c 8	696	100.0	610	6	BD211558	BD211558 Canine an
c 9	696	100.0	610	6	BD211559	BD211559 Canine an
c 10	696	100.0	610	6	AR241536	AR241536 Sequence
c 11	696	100.0	610	6	AR241537	AR241537 Sequence
c 12	696	100.0	610	6	AR254492	AR254492 Sequence
c 13	696	100.0	610	6	AR254493	AR254493 Sequence
c 14	687	98.7	405	6	AX083939	AX083939 Sequence
c 15	687	98.7	405	6	AX300436	AX300436 Sequence
c 16	610	87.6	345	6	BD211562	BD211562 Canine an
c 17	610	87.6	345	6	BD211563	BD211563 Canine an
c 18	610	87.6	345	6	AR241540	AR241540 Sequence
c 19	610	87.6	345	6	AR241541	AR241541 Sequence
c 20	610	87.6	345	6	AR254496	AR254496 Sequence
c 21	610	87.6	345	6	AR254497	AR254497 Sequence
c 22	591	84.9	838	4	AF025436	AF025436 Felis cat
c 23	586	84.2	405	6	AF068770	AF068770 Felis cat
c 24	578	83.0	405	6	SSC010088	SSC010088 Sus scrof
c 25	578	83.0	529	4	SSC133452	SSC133452 Sus scrof
c 26	571	82.0	356	4	AF091133	AF091133 Canis fam
c 27	567	81.5	405	4	ECU91947	U91947 Equus cabal
c 28	551	79.2	405	4	Z67872	Z67872 B.taurus mR
c 29	551	79.2	354	4	OAU35038	U35038 Ovis aries
c 30	541	77.7	520	4	AU35038	AF051372 Ovis aries
c 31	468	67.2	405	4	AF051372	AF051372 Felis cat
c 32	448	64.4	343	6	AX083948	AX083948 Sequence
c 33	444	63.8	421	12	SYN1L5A	M33949 Synthetic h
c 34	430	61.8	459	9	BC066282	BC066282 Homo sapi
c 35	430	61.8	816	6	CQ721603	CQ721603 cDNA encodi
c 36	430	61.8	816	6	E01639	E01639 cDNA encodi
c 37	430	61.8	816	6	E13591	E13591 cDNA encodi
c 38	430	61.8	816	9	HSIL5R	X04688 Human mRNA
c 39	430	61.8	858	6	AX766521	AX766521 Sequence
c 40	430	61.8	858	6	AX766523	AX766523 Sequence
c 41	430	61.8	4946	1	PPVIRES	Y07702 Plasmid pPV
c 42	429	61.6	405	6	CEY1N5A	CEY1N5A Sequence
c 43	426	61.2	405	9	MMU19848	U19848 Macaca mula
c 44	424	60.9	816	9	AR380691	AR380691 Sequence
c 45	424	60.9	816	9	HSBCDF1A	X12705 H.sapiens n

ALIGNMENTS

RESULT 1
BD211560
LOCUS   BD211560   402 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION   BD211560
VERSION   BD211560.1 GI:33021330
KEYWORDS   JP 2002516104-A/66.
SOURCE   Canis familiaris (dog)
  ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 402)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
  JOURNAL   Patent: JP 2002516104-A 66 04-JUN-2002;
HESKA CORP
COMMENT   OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEB SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,

Left column

PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N15/21,C12N5/10, PC
     G01N33/15,
PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC   Canine
     molecules and
     and feline immunoregulatory proteins, nucleic acid CC
     method of using the same
CC
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source   Location/Qualifiers
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ORIGIN

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Pred. No.:
Score: 1.27e-75   Length: 402
Percent Similarity: 696.00   Matches: 134
Percent Identity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00$ Indels: 0
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Qy   41  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLeuLysAsnHis 60
Db  121  CGAACTTGGCTGATAGGCGACAACCTGATGAATTCCTACTCTTGAAAAATAAAAATCAC   180

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleTyrIleAspThrLeuLysAsnGlnThrAlaHis 80
Db  181  CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACATAGAAACCAAAACTGCCCAC      240

Qy   81  GlyGluValAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysLysGlyHis   100
Db  241  GGGGAGGGCTGTGGATAAAACTATTCCAAAACTGTGTCTTTAATAAAGAACACACATAGAGC 300

Qy  101  GlnLeuLysAlaArgCysBAlaGlyIleGluArgValThrArgValPheLeuLeuLeuGln 120
Db  301  CAAAAAAAGGTGTGTGCAGGAGAGATGGAGAGTTCCTAGACTACCTGCAA            360

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
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REFERENCE   1 (bases 1 to 402)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 83 29-OCT-2002;
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US-10-787-382-5 (1-134) x AR241538 (1-402)

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Score: 696.00   Length: 402
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 6   Mismatches: 0
DB: Indels: 0
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Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
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Db   1 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTTCTTGGGGCTGCCTTANGTTTCTGCCTTT 60

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
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Db 121 CGAACTTGGCTGATAGGCGATGGGGAACCTGATGAATTCCTACTCCTGAAAATAAAATCAC 180

Qy   61 GlnLeuCysIleLeuGlyValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
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Db 181 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC 240

Qy   81 GlyGluAlaValAlaAspLysLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluGluArg 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GGGGAGGCTGTGGCAGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGGC 300

Qy 101 GlnLysGlyArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
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Db 301 CAAAAAAAAAGGTGTGCAGGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCA 360

Qy 121 ValPheLeuGlyValIleLeuAsnThrGluTrpTrpThrProGluSer 134
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Db 361 GTATTTCTTGGTGTAATAAACACCGAGTGGTGGACACCCGGAAAGT 402

RESULT 4
AR241539/c
LOCUS   AR241539   402 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6471957.
ACCESSION   AR241539
VERSION   AR241539.1 GI:27287248
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 402)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 84 29-OCT-2002;
FEATURES   Location/Qualifiers
     source   1. .402
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ORIGIN

US-10-787-382-5 (1-134) x AR241539 (1-402)

Alignment Scores:
Pred. No.:   1.27e-75
Score: 696.00   Length: 402
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
                                        Mismatches: 0

Query Match: 6   100.00%   Indels: 0
DB: Gaps: 0

US-10-787-382-5 (1-134) x AR254494 (1-402)

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Db 222 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
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Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 342 CGAACTTGGCTGATAGGCGATGGGGAACCTGATGAATTCCTACTCCTGAAAATAAAATCAC 283

Qy   61 GlnLeuCysIleLeuGlyValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
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Db 222 CAACTGTGCCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC 163

Qy   81 GlyGluAlaValAlaAspLysLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluGluArg 100
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Db 162 GGGGAGGCTGTGGCAGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGGC 103

Qy 101 GlnLysGlyArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
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Db 102 CAAAAAAAAAGGTGTGCAGGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCA 43

Qy 121 ValPheLeuGlyValIleLeuAsnThrGluTrpTrpThrProGluSer 134
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Db   42 GTATTTCTTGGTGTAATAAACACCGAGTGGTGGACACCCGGAAAGT 1

RESULT 5
AR254494
LOCUS   AR254494   402 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6482403.
ACCESSION   AR254494
VERSION   AR254494.1 GI:27303382
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 402)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 83 19-NOV-2002;
FEATURES   Location/Qualifiers
     source   1. .402
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                     /mol_type="genomic DNA"
ORIGIN

US-10-787-382-5 (1-134) x AR254494 (1-402)

Alignment Scores:
Pred. No.:   1.27e-75
Score: 696.00   Length: 402
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 6   Mismatches: 0
DB: Indels: 0
                                        Gaps: 0

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
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Db   1 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTTCTTGGGGCTGCCTTANGTTTCTGCCTTT 60

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
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Db   61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
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RESULT 6

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LOCUS       AR254495                  84 bp    DNA      linear    PAT 20-DEC-2002
DEFINITION  Sequence 84 from patent US 6482403.
ACCESSION   AR254495
VERSION     AR254495.1  GI:27303383
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 84 19-NOV-2002;
FEATURES             Location/Qualifiers
     source          1..402
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ORIGIN
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US-10-787-382-5 (1-134) x AR254495 (1-402)

Alignment Scores:

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Pred. No.:
Score:                   1.27e-75      Length:           402
Percent Similarity:      100.00%       Matches:          134
Best Local Similarity:   100.00%       Conservative:       0
Query Match:             6             Mismatches:         0
DB:                                    Indels:             0
                                       Gaps:               0
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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaThrValSerAlaPhe  20
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Db  402  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCGCTAGTGTTTCTGCCTTT 343

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis        40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  342  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTGACACTGTCTCCACTCAT     283

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis     60
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Db  282  CGAACTTGGCTGATAGGCGATGGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC   223

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysGluAspTyrLeuGln     80
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Db  222  CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGGAACCAAACTGCCCAC   163

Qy   81  ArgLeuValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluGlyArg 100
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Db  162  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAAAAACACATAGAGCGC 103

Qy  101  GlnLeuLysSerGlyCysAlaGlyGluValThrGlyTrpArgValThrLysArgPheLeuGln 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  102  CAAAAAAAAAGGTGTGCAGGAGAAAGATGGGAGGGTGACAAAGTTCCTAGACTACCTGCAA  43

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
         ||||||||||||||||||||||||||||||||||||||||||
Db   42  GTATTTCTTGGTGTGATAAACACCGAGTGGACACCCGGAAAGT   1
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RESULT 7

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LOCUS       AF331919                 610 bp    mRNA     linear    MAM 04-OCT-2001
DEFINITION  Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION   AF331919
VERSION     AF331919.1  GI:15919180
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Yang,S., Sellins,K.S., Weber,B. and McCall,C.
  TITLE     Canine interleukin-5: molecular characterization of the gene and
            expression of biologically active recombinant protein
  JOURNAL   J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
  MEDLINE   21334408
   PUBMED   11440633
REFERENCE   2  (bases 1 to 610)
  AUTHORS   Yang,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
            Prospect Parkway, Ft Collins, CO 80525, USA
FEATURES             Location/Qualifiers
     source          1..610
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
     5'UTR           1..28
     CDS             29..433
                     /note="IL-5"
                     /codon_start=1
                     /product="interleukin-5"
                     /protein_id="AAL10715.1"
                     /db_xref="GI:15919181"
                     /translation="MRMLLNLSLLALGAAAVSAFAVENPMNRLVAETLTLLSTHRTWL
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ORIGIN
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US-10-787-382-5 (1-134) x AF331919 (1-610)

Alignment Scores:

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Pred. No.:
Score:                   2.13e-75      Length:           610
Percent Similarity:      100.00%       Matches:          134
Best Local Similarity:   100.00%       Conservative:       0
Query Match:             4             Mismatches:         0
DB:                                    Indels:             0
                                       Gaps:               0
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Db   42  GTATTTCTTGGTGTGATAAACACCGAGTGGACACCCGGAAAGT   1
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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaThrValSerAlaPhe  20
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Db    1  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCGCTAGTGTTTCTGCCTTT  88

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis        40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTGACACTGTCTCCACTCAT     148

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis     60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149  CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC    208

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysGluAspTyrLeuGln     80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209  CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGGAACCAAACTGCCCAC   268

Qy   81  GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluGlyArg 100
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Db  269  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAAAACACATAGAGCGC 328

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Left column

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Qy   101  GlnLysLysArgCysAlaGlyGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
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Db   329  CAAAAAAAAGGTGTCGCAGGAGAGAAGATGGAGAGTGACAAAGTTCCTAGCTACCTCGCAA  388

Qy   121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
          ||||||||||||||||||||||||||||||||||||||||||
Db   389  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAGAAAGT  430
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RESULT 8
BD211558

LOCUS   BD211558   610 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same.
ACCESSION   BD211558
VERSION   BD211558.1 GI:33021328
KEYWORDS   .
SOURCE   Canis familiaris (dog)
  ORGANISM   Canis familiaris
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 610)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same
  JOURNAL   Patent: JP 2002516104-A 64 04-JUN-2002;
             HESKA CORP
COMMENT   Canis familiaris (dog)
  PN   JP 2002516104-A/64
  PD   04-JUN-2002
  PF   28-MAY-1999 JP 2000551002
  PR   29-MAY-1998 US 60/087306
  PI   GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
  C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
  PC   A61K39/395,
  PC   A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K16/24,C07K14/535,
  PC   C07K14/54,
  PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
  G01N33/15,
  PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC   Canine
  and feline immunoregulatory proteins, nucleic acid CC
  molecules and
  method of using the same
FEATURES   Location/Qualifiers
     source   1..610
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
ORIGIN

US-10-787-382-5 (1-134) x BD211558 (1-610)

Alignment Scores:
Pred. No.:
Score: 2.13e-75
Score: 696.00   Length: 610
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                               Gaps: 0

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Qy     1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe   20
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Db    29  ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTGTTGGGGCTGCCTANGTTCTGCCTTT   88

Qy    21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis      40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACTCAT   148

Qy    41  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   149  CGAACTTGGCTGATAGGCTATGATGGAAACCTGATGATCCTACTCCTGAAAATAAAAATCAC  208
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Right column

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Qy    61  GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuHisLysAsnGlnThrAlaHis  80
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Db   209  CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACCATTGAAAACTGCCAC        268

Qy    81  GlyGluAlaValAspLysLeuPheGlnAspMetAsnLeuSerLeuIleLysGluHisIleGluArg  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   269  GGGGAGGCCGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGGAACACATAGAGCGC   328

Qy   101  GlnLysLysArgCysAlaGlyGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
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Db   329  CAAAAAAAAGGTGTCGCAGGAGAGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTCGCAA  388

Qy   121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
          ||||||||||||||||||||||||||||||||||||||||||
Db   389  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAGAAAGT  430
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RESULT 9
BD211559/c
BD211559

LOCUS   BD211559   610 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same.
ACCESSION   BD211559
VERSION   BD211559.1 GI:33021329
KEYWORDS   .
SOURCE   Canis familiaris (dog)
  ORGANISM   Canis familiaris
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 610)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same
  JOURNAL   Patent: JP 2002516104-A 65 04-JUN-2002;
             HESKA CORP
COMMENT   Canis familiaris (dog)
  PN   JP 2002516104-A/65
  PD   04-JUN-2002
  PF   28-MAY-1999 JP 2000551002
  PR   29-MAY-1998 US 60/087306
  PI   GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
  C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
  PC   A61K39/395,
  PC   A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K16/24,C07K14/535,
  PC   C07K14/54,
  PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
  G01N33/15,
  PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC   Canine
  and feline immunoregulatory proteins, nucleic acid CC
  molecules and
  method of using the same
FEATURES   Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
ORIGIN

US-10-787-382-5 (1-134) x BD211559 (1-610)

Alignment Scores:
Pred. No.:
Score: 2.13e-75
Score: 696.00   Length: 610
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                               Gaps: 0

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Qy     1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe   20
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Left column (RESULT 10)

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Db
Qy   582 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTGCCTTT 523
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Qy    21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis       40
Db
Qy   522 GCTGTGGAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGCTCTCCACTCAT       463
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Db
Qy    41 ArgThrTrpLeuIleGlyIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db
Qy   462 CGAACTTGGCTGATAGGCGGATGGGGAACCTGATGATTCCTACTCCTGAAAATAAAATCAC 403
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Db
Qy   101 GlnLysLysArgCysAlaGlyLysGlyArgTrpArgValThrArgLysPheLeuGln       120
Db
Qy   282 CAAAAAAAAGGTGTGCAGGAGAAAGATGGCAGGTGACAAAGTTCCTAGACTACCTGCAA   223
Db
Qy   121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                     134
Db
Qy   222 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGGAAAGT                   181
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RESULT 10

LOCUS   AR241536   610 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION AR241536
ACCESSION   AR241536
VERSION   AR241536.1   GI:27287245
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 610)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wondering,R.S.
  TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 80 29-OCT-2002;
FEATURES   Location/Qualifiers
     source   1..610
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 696.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6

US-10-787-382-5 (1-134) x AR241536 (1-610)

DB: 2.13e-75
                                                       Length: 610
                                                       Matches: 134
                                                       Conservative: 0
                                                       Mismatches: 0
                                                       Indels: 0
                                                       Gaps: 0

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Qy     1 MetArgMetLeuLeuAsnLeuSerLeuValAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
Db
Qy     1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTGCCTTT  88
Db    29 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis       40
Db    89 GCTGTGGAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGCTCTCCACTCAT      148
Qy    41 ArgThrTrpLeuIleGlyIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db   149 CGAACTTGGCTGATAGGCGGATGGGGAACCTGATGATTCCTACTCCTGAAAATAAAATCAC 208
Qy    61 GlnLysLysArgCysAlaGlyLysGlyArgTrpArgValThrArgLysPheLeuGln       80
Db   209 CAAACTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC  268
Qy    81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysSerGlnHisIleGluArg 100
Db    81 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC  268
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Right column (RESULT 11 / RESULT 12)

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Db   269 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   101 GlnLysLysArgCysAlaGlyLysGlyArgTrpArgValThrArgLysPheLeuGln       120
Db   329 CAAAAAAAAGGTGTGCAGGAGAAAGATGGCAGGTGACAAAGTTCCTAGACTACCTGCAA   388
Qy   121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                     134
Db   389 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGGAAAGT                   430
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RESULT 11

LOCUS   AR241537/c   610 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION AR241537
ACCESSION   AR241537
VERSION   AR241537.1   GI:27287246
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 610)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wondering,R.S.
  TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 82 29-OCT-2002;
FEATURES   Location/Qualifiers
     source   1..610
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 696.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 6

US-10-787-382-5 (1-134) x AR241537 (1-610)

DB: 2.13e-75
                                                       Length: 610
                                                       Matches: 134
                                                       Conservative: 0
                                                       Mismatches: 0
                                                       Indels: 0
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Qy     1 MetArgMetLeuLeuAsnLeuSerLeuValAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
Db
Qy    21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis       40
Db   582 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTGCCTTT 523
Db
Qy   522 GCTGTGGAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGCTCTCCACTCAT       463
Db
Qy    41 ArgThrTrpLeuIleGlyIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db   462 CGAACTTGGCTGATAGGCGGATGGGGAACCTGATGATTCCTACTCCTGAAAATAAAATCAC 403
Db
Qy   101 GlnLysLysArgCysAlaGlyLysGlyArgTrpArgValThrArgLysPheLeuGln       120
Db   282 CAAAAAAAAGGTGTGCAGGAGAAAGATGGCAGGTGACAAAGTTCCTAGACTACCTGCAA   223
Qy   121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                     134
Db   222 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGGAAAGT                   181
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RESULT 12

LOCUS   AR254492   610 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION Sequence 80 from patent US 6482403.

ACCESSION   AR254492
VERSION   AR254492.1 GI:27303380
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 610)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wondering,R.S.
  TITLE   Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 80 19-NOV-2002;
FEATURES
     source   1..610
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:
Score: 2.13e-75   Length: 610
Percent Similarity: 696.00   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                         Gaps: 0

US-10-787-382-5 (1-134) x AR254492 (1-610)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20

Qy   29 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 88
Db   29 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 88

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
Db   89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACTCAT 148

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db 149 CGAACTTGGCTGATTAGGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 208

Qy   61 GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 209 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCCAC 268

Qy   81 GlyGluAlaValAspGlyLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
Db 269 GGGGAGGCTGTGGATGGAAAACTTCTTAATAAAAGAACACATAGAGCGC 328

Qy 101 GlnLysGlySAsrgCysAlaGlyGlnArgTrpArgValThrIleLysPheLeuAspTyrLeuGln 120
Db 329 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 388

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 389 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 430

US-10-787-382-5.rge

RESULT 13
LOCUS   AR254493/c
DEFINITION Sequence 82 from patent US 6482403.
ACCESSION   AR254493
VERSION   AR254493.1 GI:27303381
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 610)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wondering,R.S.
  TITLE   Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 82 19-NOV-2002;
FEATURES
     source   1..610
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

AR254493 610 bp DNA linear PAT 20-DEC-2002

Alignment Scores:
Pred. No.:
Score: 2.13e-75   Length: 610
Percent Similarity: 696.00   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                         Gaps: 0

US-10-787-382-5 (1-134) x AR254493 (1-610)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
Db   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
Db 522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACTCAT 463

Db 582 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 523

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db 462 CGAACTTGGCTGATTAGGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 403

Qy   61 GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 402 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCCAC 343

Qy   81 GlyGluAlaValAspGlyLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
Db 342 GGGGAGGCTGTGGATGGAAAACTTCTTAATAAAAGAACACATAGAGCGC 283

Qy 101 GlnLysGlySAsrgCysAlaGlyGlnArgTrpArgValThrIleLysPheLeuAspTyrLeuGln 120
Db 282 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 223

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
Db 222 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 14
LOCUS   AR300436
DEFINITION Sequence 1 from patent US 6537781.
ACCESSION   AR300436
VERSION   AR300436.1 GI:31687875
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 405)
  AUTHORS   Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.
  TITLE   Methods and compositions concerning canine interleukin 5
  JOURNAL   Patent: US 6537781-A 1 25-MAR-2003;
FEATURES
     source   1..405
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

AR300436 405 bp DNA linear PAT 12-JUN-2003

Alignment Scores:
Pred. No.:
Score: 1.61e-74   Length: 405
Percent Similarity: 687.00   Matches: 133
Best Local Similarity: 99.25%   Conservative: 0
Query Match: 99.25%   Mismatches: 1
DB: 6   Indels: 0
                                         Gaps: 0

US-10-787-382-5 (1-134) x AR300436 (1-405)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
Db   1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 60

RESULT 15

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LOCUS       AX083939         405 bp      DNA      linear    PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0111049.
ACCESSION   AX083939
VERSION     AX083939.2  GI:14532940
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1
  AUTHORS   Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.
  TITLE     Methods and compositions concerning canine interleukin 5
  JOURNAL   Patent: WO 0111049-A 1 15-FEB-2001;
            IDEXX LABORATORIES, INC. (US)
COMMENT     On Jun 24, 2001 this sequence version replaced gi:13185501.
FEATURES             Location/Qualifiers
     source          1..405
                     /organism="Canis familiaris"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9615"
ORIGIN
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Qy    21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis    40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCCCACTCAT   120

Qy    41  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CGAACTTGGCTGATAGGCCATGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAATCAC   180

Qy    61  GlnLeuCysIleLeuLysGluValPheGlnGlyIleAspAsnThrLeuLysGlnThrAlaHis    80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CAACTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAGAACACCAAACTGCCCAC   240

Qy    81  GlyGluAlaValAlaAspLysSerPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg   100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GGGGAGGCTGTGGATAAAACTAATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC   300

Qy   101  GlnLysLysArgCysValAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA   360

Qy   121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
          ||||||||||||||||||||||||||||||||
Db   361  GTATTTCTTGGTGTGTAATAAACACCCAGTGACAATGGAAAGT   402
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US-10-787-382-5 (1-134) x AX083939 (1-405)

Alignment Scores:
Pred. No.:              1
Score:              687.00
Percent Similarity:  99.25%
Best Local Similarity: 99.25%
Query Match:         98.71%
DB:                     6

                     Length:        405
                     Matches:       133
                     Conservative:    0
                     Mismatches:      1
                     Indels:          0
                     Gaps:            0
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Qy     1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaThrTyrValSerAlaPhe   20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGAGAATGCTTCTCAAATTTGAGTTTGCTAGCCTCTGGGGCTGCCTARGTTTCTGCCTTT   60

Qy    21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis   40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GCTGTGAAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCCCACTCAT  120

Qy    41  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CGAACTTGGCTGATAGGCTGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAATCAC  180

Qy    61  GlnLeuCysIleLeuLysGluValPheGlnGlyIleAspAsnThrLeuLysGlnThrAlaHis   80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CAACTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACACCAAAACTGCCCAC  240
```

```
Qy    81  GlyGluAlaValAlaAspLysSerPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg  100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GGGGAGGCTGTGGATAAAACTAATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC  300

Qy   101  GlnLysLysArgCysValAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA  360

Qy   121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
          ||||||||||||||||||||||||||||||||
Db   361  GTATTTCTTGGTGTGTAATAAACACCCAGTGACAATGGAAAGT  402
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 6, 2005, 19:27:15 ; Search time 366.482 Seconds
          (without alignments)
          2164.487 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLLNLSLLALGAAYVSAF..........FLDYLQVFLGVINTEWTPES 134

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                Ygapop 10.0 , Ygapext 0.5
                Pgapop 6.0 , Pgapext 7.0
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Searched: 4390206 seqs, 295987067 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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           13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	696	100.0	402	3	AAZ55548	Canine ma
c	2	696	100.0	402	3	AAZ55551	Canine ma
c	3	696	100.0	610	3	AAZ55549	Canine in
c	4	696	100.0	610	3	AAZ55546	Canine in
c	5	687	98.7	405	4	AAF74300	Canine in
	6	610	87.6	345	3	Aaz55550	Canine ma
	7	610	87.6	345	3	Aaz55551	Canine ma
	8	591	84.9	838	3	Aaz44265	Porcine I
	9	541	77.7	520	2	Aat50755	Ovine IL-
	10	536	77.0	399	2	Aat50756	Ovine IL-
	11	513	73.7	393	4	Aaf74306	Canine in
	12	430	61.8	816	4	Aaa34857	Human ade
	13	430	61.8	816	3	Aaa13338	Human int
	14	430	61.8	816	3	Aaf20979	Human low
	15	430	61.8	816	3	Adg33104	Human DNA
	16	430	61.8	858	9	Abz96673	Human nuc
	17	430	61.8	816	10	Acf63368	Human int
	18	430	61.8	520	2	Adp56009	Human PRO
	19	430	61.8	4057	11	Aal61293	hIL5-P2-P
	20	430	61.8	858	9	Aal61294	hIL5-P30-
	21	430	61.8	4057	3	Aaa34858	Human ade
	22	430	61.8	4057	10	Aaf20980	Human low
	23	430	61.8	4057	11	Abz96674	Human nuc
	24	430	61.8	4057	11	Abd20523	Human pul
	25	430	61.8	4057	11	Abd20522	Human pul
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	27	424	60.9	816	11	Adi31910	Canine cDN
	28	420	60.3	402	1	Aan81380	A human B
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	30	413.5	59.4	864	9	Aal61295	hIL5.36 v
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	32	376	54.0	402	2	Aat14921	T cell re
	33	376	54.0	1534	2	Aat88013	Murine In
	34	376	54.0	1623	2	Aat14925	T cell re
	35	376	54.0	1623	2	Aav64062	Plasmid p
	36	375	53.9	1533	1	Aan82431	B cell di
	37	370	51.9	370	1	Aan91647	Synthetic
	38	361	51.9	1945	10	Adb53890	Primary r
	39	361	51.0	481	1	Aan80461	Clone 115
	40	355	51.0	377	2	Aav01595	T cell re
	41	351	50.4	348	2	Aat14922	T cell re
	42	347	49.9	385	2	Aaa43842	Human sec
	43	346	49.7	385	2	Aat14923	T cell re
	44	343	49.3	342	2	Aat14924	T cell re
	44	342	49.1	339	2	Aat14924	T cell re
	45	332.5	47.8	381	3	Aac68867	Modified

ALIGNMENTS

RESULT 1
AAZ55548

ID   AAZ55548 standard; cDNA; 402 BP.
XX
AC   AAZ55548;
XX
DT   14-MAR-2000 (first entry)
XX
DE   Canine interleukin-5 (IL-5) cDNA coding region.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; as.
XX
OS   Canis familiaris.
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58219.

Left column

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XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 225; 264pp; English.
XX
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SQ   Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;
XX

US-10-787-382-5 (1-134) x AA255548 (1-402)

Alignment Scores:
Pred. No.:
Score:                   7.02e-79
Percent Similarity:      696.00          Length:          402
Best Local Similarity:   100.00%         Matches:         134
Query Match:             100.00%         Conservative:    0
                         100.00%         Mismatches:      0
DB:                      3               Indels:          0
                                         Gaps:            0

Qy    1  MetArgThrMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaIleTyrValSerAlaPhe   20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGAGAACTATGCTTCTCAGATTTGAGTTTGCTAGCCTCTGGGGCTGCCTAGTTTCTGCCTTT      60

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis          40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT         120

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis          60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC         180

Qy   61  GlnLeuCysIleLysGluGlyAspSerLeuLysAsnLeuSerLeuLysGluGluArg            80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CAAACTGTGCATTAAAGAGGGTATAGACACATTGAAGAACCTGAGCCTGAAGGAAGAG         240

Qy   81  GlyGluValAlaValAlaAspLysAsnThrGlyThrProLeuArg                        100
         |||||||||||||||||||||||||||||||||||||||||||||
Db  241  GGGGAGGTCGTGGGATAAACTATTCCAAAACTTGTCTTAAT                            300

Qy  101  GlnLysLysArgCysSerAlaGlyGluArgTrpApArgValThrArgPheLeuAspArgTyrLeuGln  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  CAAAAAAAAAGGTGTCGCAGGAGAAAGATGGGAAGATGGAC                            360

Qy  121  ValPheLeuGlyValIleAsnThrGlyThrTrpThrProGluSer                        134
         |||||||||||||||||||||||||||||||||||||||||
Db  361  GTATTTCTTGGTGTAATAAACCGAGTGGACACCGGAAAGT                            402
```

Right column

```
DB
XX
OS   Canine interleukin-5 (IL-5) cDNA coding region complement.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
```

```
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 226; 264pp; English.
XX
```

```
SQ   Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;
XX

Claim 1h; Page 226; 264pp; English.

US-10-787-382-5 (1-134) x AA255549 (1-402)

Alignment Scores:
Pred. No.:
Score:                   7.02e-79
Percent Similarity:      696.00          Length:          402
Best Local Similarity:   100.00%         Matches:         134
Query Match:             100.00%         Conservative:    0
                         100.00%         Mismatches:      0
DB:                      3               Indels:          0
                                         Gaps:            0

Qy    1  MetArgThrMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaIleTyrValSerAlaPhe   20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGAGAAGTCTTCTGAAATTTGGTAGCTTCTGGGGCTGCCTARTGTTTCTGCCTTT            402

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis          40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT         283

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis          60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  342  CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC         283

Qy   61  GlnLeuCysIleLysGluGlyValPheGlnGlyIleIleGluAspThrLeuLysAsnGlnThrAlaHis  80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  282  CGAACTGTGCATTAAAGAAGAAGTTTTTCAGGGTATAGACACATTGAAGAGACCAAACTGCCAC    223

Qy  222  CAACTGTGCATTAAAGAAGAAGTTTTTCAGGGTATAGACACATTGAAGAGACCAAACTGCCAC      163
```

```
Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  162 GGGGAGGCGTGTGGAATAAAACTTGTCTTAATAAAAGAACACATAGAGCGC 103

Qy  101 GlnLysGlyArgCysAlaGlyArgValThrLysPheLeuAspTyrLeuGln 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  102 CAAAAAAAAGGTGTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACCTACCTGCAA 43

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
        ||||||||||||||||||||||||||||||||||||||||||
Db   42 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1
```

RESULT 3
AAZ55546

```
ID   AAZ55546 standard; cDNA; 610 BP.
XX
AC   AAZ55546;
XX
DT   14-MAR-2000 (first entry)
XX
DE   Canine interleukin-5 (IL-5) cDNA.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             29..433
FT                   /*tag= a
FT                   /product= "Canine IL-5"
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;  99WO-US011942.
XX
PR   29-MAY-1998;  98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G,  Yang S,  Dreitz MJ,  Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58219.
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 223-224; 264pp; English.
XX
CC   Sequences AAZ55546-255551 represent cDNA sequences encoding canine
CC   interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC   feline Flt-3 ligand), canine or feline CD40, canine or feline CD40
CC   ligand), canine IL-5, canine interferon-alpha (IFN-alpha), feline
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   of activity, while the antibodies may be used in detection, and in drug
CC   targeting.
XX
SQ   Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                 1.26e-78        Length:          610
Score:                     696.00          Matches:         134
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               100.00%         Indels:          0
DB:                        3               Gaps:            0
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US-10-787-382-5 (1-134) x AAZ55546 (1-610)

```
Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuAlaLeuAlaLeuAlaThrTyrAlaValSerAlaPhe 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  29 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTCCCTATGTTTCTGCCTTT 88

Qy  21 AlaValGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgThrHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  89 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 148

Qy  41 ArgThrThrProLeuIleLeuGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 149 CGAACTTGGCTCAGTAAGGCCGATGGGAACCTGAATGATCTCCTACTCCTGAAAATAAAATCAC 208

Qy  61 GlnLeuCysIleLeuGluGlyValPheGlnGlyIleAspAspThrLeuLysAsnGlnThrAlaHis 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 209 CAACTGTGCATTGAAGGAGGTTTTTCAGGGTATAGACAATGGAAGACCAAACTGCCCAC 268

Qy  81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 269 GGGGAGGCGTGTGGAATAAAACTTGTCTTAATAAAAGAACACATAGAGCGC 328

Qy 101 GlnLysGlyArgCysAlaGlyArgValThrLysPheLeuAspTyrLeuGln 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 329 CAAAAAAAAGGTGTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACCTACCTGCAA 388

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
        ||||||||||||||||||||||||||||||||||||||||||
Db 389 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 430
```

RESULT 4
AAZ55547/c

```
ID   AAZ55547 standard; cDNA; 610 BP.
XX
AC   AAZ55547;
XX
DT   14-MAR-2000 (first entry)
XX
DE   Canine interleukin-5 (IL-5) cDNA complement.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement(178..582)
FT                   /*tag= a
FT                   /product= "Canine IL-5"
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;  99WO-US011942.
XX
PR   29-MAY-1998;  98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G,  Yang S,  Dreitz MJ,  Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58219.
```

XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
    useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS Claim 1h; Page 224-225; 264pp; English.
XX
CC Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC feline Flt-3 ligand, canine IL-5, feline CD40, canine or feline CD154 (CD40
CC ligand), canine IL-5, feline interferon-alpha (IFN-alpha),
CC and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC nucleotides which encode these immunoregulatory proteins. The proteins,
CC their associated nucleic acids, specific antibodies and inhibitors may be
CC used as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targeting.
XX
SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   Length: 610
Score: 1.26e-78   Matches: 134
Percent Similarity: 696.00   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
                       100.00%   Gaps: 0
                       3

US-10-787-382-5 (1-134) x AAZ55547 (1-610)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuLeuLeuGlyAlaAlaTyrValSerAlaPhe 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 582 ATGAGAAATGCTTCTGAATTTGAGTTNGCTAGCTCCTTGGGGCGCGCCTANGTTNCTGCCTTT 523

Qy   21 AlaValAlaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 522 GCTGTGAGAAAATCCCATGAATAGACNTGGTGCGCAGAGAACCTTGACACNGCTCTCCACTCAT 463

Qy   41 ArgThrTrpLeuIleLeuGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 462 CGAACTTGGCTCGATAGGGCGATGGGAACCTGACACNCTCCTACTCCCTGAAAATAAAAATCAC 403

Qy   61 GlnLeuCysIleLeuLysGlyValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402 CAACTGTGCATTAAAGAAGGTTTTTCAGGGTATAGACACNATTGAAGAACCAAAACTGCCCAC 343

Qy   81 GlyGluAlaValAspGlyLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleLeuGluArg 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 342 GGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTNAATAAAGAACACATAGAGCGC 283

Qy 101 GlnLysLysArgCysSerAlaGlyGlyValThrIleLysValPheLeuAspTyrLeuGln 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 282 CAAAAAAAAAGGTGTGCAGGAGAAAGATGGGGACTGGGACAAAAAGTTCCTAGACTACATAGAGCGC 223

Qy 121 ValPheLeuGluGlyValIleAsnThrGluTrpThrProGluSer 134
        ||||||||||||||||||||||||||||||||||||||||||||
Db 222 GTATTTCTTGGGTGTAATAAACACCGAGTGGGACACCCGAAAGT 181

RESULT 5
ID AAF74300 standard; DNA; 405 BP.
XX
AC AAF74300;
XX
DT 04-MAY-2001 (first entry)
XX

DE Canine interleukin-5 coding sequence #1.
XX
OS Canis sp.
XX
KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; ds.
XX
PN WO2001I1049-A2.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021651.
XX
PR 10-AUG-1999; 99US-00371615.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Guo H, Lawton R, Mermer B, Alyappa AP;
XX
PS Claim 31; Page 46; 48pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is one
CC version of the IL-5 coding sequence shown in the specification
XX
DR WPI; 2001-191542/19.
DR P-PSDB; AAB72615.
XX
PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   Length: 405
Score: 9.89e-78   Matches: 133
Percent Similarity: 687.00   Conservative: 0
Best Local Similarity: 99.25%   Mismatches: 1
Query Match: 99.25%   Indels: 0
                       98.71%   Gaps: 0
                       4

US-10-787-382-5 (1-134) x AAF74300 (1-405)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuLeuLeuGlyAlaAlaTyrValSerAlaPhe 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAGAAATGCTTCTGAATTTGAGTTNGCTAGCTCCTTGGGGCGCGCCTANGTTNCTGCCTTT 60

Qy   21 AlaValAlaGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GCTGTGAGAAAATCCCATGAATAGACNTGGTGCGCAGAGAACCTTGACACNGCTCTCCACTCAT 120

Qy   41 ArgThrTrpLeuIleLeuGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CGAACTTGGCTCGATAGGGCGATGGGAACCTGACACNCTCCTACTCCCTGAAAATAAAAATCAC 180

Qy   61 GlnLeuCysIleLeuLysGlyValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CAACTGTGCATTAAAGAAGGTTTTTCAGGGTATAGACACNATTGAAGAACCAAAACTGCCCAC 240

Qy   81 GlyGluAlaValAspGlyLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleLeuGluArg 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTNAATAAAGAACACATAGAGCGC 300

Qy 101 GlnLysLysArgCysSerAlaGlyGlyValThrIleLysValPheLeuAspTyrLeuGln 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CAAAAAAAAAGGTGTGCAGGAGAAAGATGGGGACTGGGACAAAAAGTTCCTAGACTACCTGCAA 360

Qy 121 ValPheLeuGluGlyValIleAsnThrGluTrpThrProGluSer 134
        ||||||||||||||||||||||||||||||||||||||||||||
Db 361 GTATTTCTTGGGTGTAATAAACACCGAGTGGGACACCCGAAAGT 402

RESULT 6

```
AA255550
ID   AA255550 standard; cDNA; 345 BP.
XX
AC   AA255550;
XX
DT   14-MAR-2000  (first entry)
XX
DE   Canine mature interleukin-5 (IL-5) cDNA.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wondering RS;
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 226-227; 264pp; English.
XX
CC   Sequences AA255546-255551 represent cDNA sequences encoding canine
CC   interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC   feline Flt-3 ligand, canine IL-5, canine or feline CD40, canine or
CC   feline CD154 (CD40 ligand), canine IL-13, feline interferon-alpha (IFN-alpha)
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSP), and
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   of activity, while the antibodies may be used in detection, and in drug
CC   targeting.
XX
SQ   Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;
```

Alignment Scores:

```
Pred. No. :
Score:               4.85e-68       Length:        345
Percent Similarity:  610.00         Matches:       115
Best Local Similarity: 100.00%      Conservative:  0
Query Match:         100.00%        Mismatches:    0
DB:                  3              Indels:        0
                     87.64%         Gaps:          0
```

US-10-787-382-5 (1-134) x AA255550 (1-345)

```
Qy   40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGlnAsnLysAsn 59
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 TTTGCGTGTAGGAAAAATCCATGAAATAGACTGGTGTGGCAGAGACCTTGACACTGCTCTCCACT 120

Qy   20 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 39
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TTTGCGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Qy   61 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGlnAsnLysAsn 79
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGAACTTGGCTGATAGGCGCCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAT 120
```

Alignment Scores:

```
Qy    60 HisGlnLeuCysIleIleLysGluValPheGlnGlyIleIleAsnAspThrLeuLysAsnGlnThrAla  79
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACAATTGAACAAACTGCC 180

Qy    80 HisGlyGluAlaValAspProLysGluPheGlnAsnLeuSerLeuIleLysGluHisIleGlu  99
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CACGGGGAGGCGGTGGGATAAACTAATTCCAAAACTTGTCTTTAATAAAAAGACACATAAG 240

Qy   100 ArgGlnLysGlyArgCysAlaGlyGluArgThrProArgValThrrlysPhePheLeuAspTyrLeu 119
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCCCAAAAAAAAAGGGTGTGCAGGAGGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300

Qy   120 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
          |||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAAGTATTTCTTCGTGTGTAATAAAACACCCGAGTGGACACCGGAAAGT 345
```

```
RESULT 7
AA255551/c
ID   AA255551 standard; cDNA; 345 BP.
XX
AC   AA255551;
XX
DT   14-MAR-2000  (first entry)
XX
DE   Canine mature interleukin-5 (IL-5) cDNA complement.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wondering RS;
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 228; 264pp; English.
XX
CC   Sequences AA255546-255551 represent cDNA sequences encoding canine
CC   interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC   feline Flt-3 ligand, canine IL-5, canine or feline CD40, canine or
CC   feline CD154 (CD40 ligand), canine IL-13, feline interferon-alpha (IFN-alpha)
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSP), and
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   of activity, while the antibodies may be used in detection, and in drug
CC   targeting.
XX
SQ   Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;
```

Alignment Scores:

```
Pred. No.:
Score:                         4.85e-68
Percent Similarity:            610.00
Best Local Similarity:         100.00%
Query Match:                   100.00%
                               87.64%

Length:      345
Matches:     115
Conservative: 0
Mismatches:   0
Indels:       0
Gaps:         0

US-10-787-382-5 (1-134) x AA255551 (1-345)

Qy     20 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr 39
                                                             
Db    345 TTTGCTGTAGAAAATCCAATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy     40 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 59
                                                             
Db    285 CATCGAACTTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy     60 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 79
                                                             
Db    225 CACCAAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACCATTGAAGAACCAAACTGCC 166

Qy     80 HisGlyGluAlaValAlaSerProLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 99
                                                             
Db    165 CACGGGGGAGGCTGTGGGGATAAAACTTGTCTTAATAAAAAGAACACAATAGAG 106

Qy    100 ArgGlnLysLysArgCysSerAlaGlyTrpValThrLysPheLeuAspTyrLeu 119
                                                             
Db    105 CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTAAAAAGTTCCTAGACTACTACCTG 46

Qy    120 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
                                                             
Db     45 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 8
ID     AA244265 standard; DNA; 838 BP.
AC     AA244265;
XX
DT     31-MAR-2000 (first entry)
XX
DE     Porcine IL-5 DNA.
XX
KW     Pig; vaccine; cysticercosis; protective antigen; cc1; cc3; cc4;
KW     tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.
OS     Sus scrofa.
```

```
CC     simple and convenient, the physical and chemical properties of the
CC     vaccine are stable, and the vaccine is easy to store and transport, and
CC     possesses effective immunological protective function for human and pig
CC     cysticercosis. This sequence represents the pig IL-5 gene used in the
CC     method of the invention
XX
SQ     Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                         4.37e-65
Percent Similarity:            591.00
Best Local Similarity:         93.28%
Query Match:                   85.07%
DB:                            84.91%

Length:      838
Matches:     114
Conservative: 11
Mismatches:   9
Indels:       0
Gaps:         0

US-10-787-382-5 (1-134) x AA244265 (1-838)

Qy      1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
                                                             
Db     45 ATGAGAAATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGGGCTGCCTTANGTTTCTGCCATT 104

Qy     21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
                                                             
Db    105 GCTGTACAAAATCCCATGAATAGAGCTGGTGGCAGAGACCTTGGCACTGCTCTCCACTCAT 164

Qy     41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
                                                             
Db    165 CGAACTTGCTGATAGGCGACGGGAACCTGATGATTCCTACTCCTGAACAATAAGAATCAC 224

Qy     61 GlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHis 80
                                                             
Db    225 CAACTGTGCATTGAAGAAGTCTTTCAGGGTATAGACACTTAAAAGAATCGCACGTGTGCCG 284

Qy     81 GlyGluAlaValAlaSerProLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
                                                             
Db    285 GGGGAGTGCTGTGGAAAAAGCTTTCCGAAACTTGTCTTAATAAAAAGAACACAATAGACCGC 344

Qy    101 GlnLysLysArgCysSerAlaGlyTrpValThrLysPheLeuAspTyrLeuGln 120
                                                             
Db    345 CAAAAAAAAAGTGTGCAGGAGAAACAATGGAGAGTAAAAAGTTCCTAGACTACTACCTGCAA 404

Qy    121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
                                                             
Db    405 GTGTTTCTTGGTGTAATAAACACTGAGTGGACAATGGAAAGT 446

RESULT 9
ID     AAT50755 standard; DNA; 520 BP.
AC     AAT50755;
XX
DT     17-OCT-2003 (revised)
DT     24-SEP-1997 (first entry)
XX
DE     Ovine IL-5 gene.
XX
KW     Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW     livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW     immunosuppression; allergy; reproductive system; growth; early maturity;
KW     antibody; diagnosis; immunopotentiator;
KW     early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW     secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.
OS     Ovis aries.
```

```
DB:

Query Match:                   3

Gaps:         0

AA244265;

13-OCT-1999.

CNI23133-A.

29-JAN-1999;    99CN-00113447.
29-JAN-1999;    99CN-00113447.

WPI; 2000-087904/08.

Sun S, Dai J;

(UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.

Nucleic acid vaccine for cysticercosis co-contracted by human and pig.

Claim 3; Page 9; 21pp; Chinese.

This invention describes a novel nucleic acid vaccine for preventing and
curing human and pork cysticercosis. The invention involves the formation
of a eukaryotic expression plasmid from fusion transcript expression unit
consisting of three protective antigen genes (cC1, cC3 and cC4) of pig
tenial cysticercus and coexpression unit of related cell factor gamma
interferon (IFN-gamma) and pork interleukin 5 (IL-5)] genes. The
production and purification process of said nucleic acid vaccine is
```

```
Ovis aries.

Key               Location/Qualifiers
CDS               46..444
                  /*tag= a
exon              46..183
                  /product= "Ovine_IL-5"
                  /*tag= b
                  /number= 1
```

FT   exon   184..216
FT   /*tag= c
FT   exon   217..345
FT   /*tag= 2
FT   /number= 2
FT   exon   346..480
FT   /*tag= 3
FT   /number= 3
FT   exon   /*tag= e
FT   /number= 4
XX
PA   (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PN   WO9700321-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-AU000360.
XX
PR   14-JUN-1995;   95AU-00003502.
PR   27-OCT-1995;   95AU-00006244.
XX
PI   Seow H, Wood P;
XX
DR   WPI; 1997-077528/07.
DR   P-PSDB; AAW08479.
XX
PS   Claim 6; Page 39-40; 78pp; English.
XX
PT   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT   adjuvants and to treat or prevent microbial infections in livestock.
CC   The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
CC   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC   livestock (esp. cows and sheep), particularly where the animals are
CC   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC   subunit or synthetic peptide vaccines). They may also be used to treat
CC   cancer, immunosuppression and allergy, to enhance/suppress the
CC   reproductive system and to promote growth or early maturity. Optionally
CC   interleukin can be delivered from constructs or delivery cells and
CC   antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC   infection. The interleukins are immunopotentiators, especially IL-5
CC   promotes growth of early haematopoietic progenitor cells and generation
CC   of cytotoxic cells from thymocytes, also it stimulates production and
CC   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC   induces production of gamma-interferon by, and proliferation of, T and NK
CC   cells and increases the (non-)specific cytolytic lymphocyte response. The
CC   genetic constructs can also be used for in vitro production of IL-5 or -
CC   12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:

Score: 541.00   Length: 520
Pred. No.:   5.08e-59   Matches: 105
Percent Similarity: 90.23%   Conservative: 15
Best Local Similarity: 78.95%   Mismatches: 13
Query Match: 77.73%   Indels: 0
DB: 2   Gaps: 0

US-10-787-382-5 (1-134) x AAT50755 (1-520)

Qy   2 ArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPheAla   21
          ||||||||:||::||::|||::|||::||||||||
Db   2 AGAATGCATTCGGCGTTGACCTTGGGTAGCTCTTGGAGCTGCCTATGTTTGTGCCAATGCT   43

Qy   22 ValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArg   41
          |||||::|||:|||
Db   43 GTGGAAAATCCAATGAATAGACTGGTGCCAGAGACCCTGACCACTGCTCTCCAGGCATCA   103

Qy   103 GTAGAAAATACCAATGAATAGACTGGTGCCAGAGACCCTGACCACTGCTCTCCAGGCATCAA   162

Qy   42 ThrTrpLeuIleGlyAspGlyAsnGlyAsnGlyMetIleProThrProGluAsnLysAsnHisGln   61
          ||| |||||||||
Db   163 ACTTCGCTGATAGGTGAATGGGAACTTGATGAATTCCTTCACTCCTCAGCATACAAAATCACCAA   222

CC cells and increases the (non-)specific cytolytic lymphocyte response. The
CC genetic constructs can also be used for in vitro production of IL-5 or -
CC 12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 399 BP; 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;

US-10-787-382-5 (1-134) x AAF50756 (1-399)

Alignment Scores:
Pred. No.:   1
Score: 1.52e-58   Length: 399
Percent Similarity: 90.15%   Matches: 104
Best Local Similarity: 78.79%   Conservative: 15
Query Match: 2   Mismatches: 13
DB: Indels: 0
                                      Gaps: 0

Qy   3 MetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPheAlaVal 22
        |||.|: ||||||::|::|| |||| ||||||||.|||||..||||||||.:||
Db   1 ATGCAtCTtGGCTTTGACCTTGGTAGCTtCTTGGAGtTGCCTAaGTTTGTGCCAAATGCTGTA 60

Qy 23 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArgThr 42
        |||.||:
Db 61 GAAAAGTACCAATGAATAGACTGGTTGGCAGAGACCTTGACACTTGCTCTCCACGCCATCAAACT 120

Qy 43 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 62
        ||||||||||||||:::::
Db 121 CTGGCTGATAGGTGACGGAACTTGATGATTCCTACTCCTCCAGCATACAAATCACCAACTA 180

Qy 63 CysIleLeuTyrSerGluValPheGlnIleLysAspThrLeuGlnThrArgLeuHisGlyGlu 82
        |||||||||.|||||||||||::|
Db 181 TGCATTGAAGAAGTCTTTCAGGGAATAGACACATTGAAGAAATCACTGACACAAGGGAT 240

Qy 83 AlaValAsnProLeuPheGlnAsnLeuSerLeuIleLysLysGluHisIleGluArgGlnLys 102
        |||
Db 241 GCTGTGAAAAAAATATTCCGAAACTTGTCTTTAATAAAAGAATACATAGACCTCCAAAAA 300

Qy 103 LysArgCysSerAlaGlyLeuArgThrArgValThrLysPheLeuAspTyrLeuGlnValPhe 122
        :::::||
Db 301 AGGAAGTGTGGAGCAGGAAGAAGATGGAGAGTGAAAACAAATTCCTCGACTACCTGCAAGTTTTC 360

Qy 123 LeuGlyValIleAsnThrGluTrpProProGluSer 134
        |||||||
Db 361 CTTGGTGTGATAAACACAGAGTGGACCAGGAAAGC 396

RESULT 11
AAF74306
ID AAF74306 standard; DNA; 393 BP.
XX
AC AAF74306;
XX
DT 04-MAY-2001 (first entry)
XX
DE Canine interleukin-5 coding sequence #3.
XX
KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; de.
XX
OS Canis sp.
XX
PN WO20011049-A2.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021651.
XX
PR 10-AUG-1999; 99US-0371615.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Guo H, Lawton R, Mermer B, Alyappa AP;
XX
DR WPI; 2001-191542/19.
XX

PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
PS Claim 1; Page 35; 48pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is one
CC version of the IL-5 coding sequence shown in the specification
XX
SQ Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;

US-10-787-382-5 (1-134) x AAF74306 (1-393)

Alignment Scores:
Pred. No.:   1
Score: 1.24e-55   Length: 393
Percent Similarity: 100.00%   Matches: 95
Best Local Similarity: 97.94%   Conservative: 2
Query Match: 4   Mismatches: 0
DB: Indels: 0
                                      Gaps: 0

Qy 35 ThrLeuLeuSerThrHisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThr 54
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACACTGCTCTCCACTCATCGAACTTGGCTGATAGGTGACGGAAACTTGATGATTCCTACT 60

Qy 55 ProGluAsnLysAsnHisGlnLeuCysIleLeuTyrSerGluValPheGlnIleLysAspThrLeu 74
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 CCTGAAAATAAAAATCACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTG 120

Qy 75 LysAsnGlnThrAlaHisGlyGluAlaValAlaAspLysValSerPheGlnAsnLeuSerLeuIle 94
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AAGAACCAAACTGCCCACGGGGAGGCTGTGGATAAAACTATTCCAAACTTGTCTTTAATA 120

Qy 95 LysGluHisIleGluArgGlnLysLysArgCysSerAlaGlyLeuArgThrArgValThrLys 114
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 AAAGAACACATAGAGCGCCAAAAAAAGAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAG 240

Qy 115 PheLeuAspTyrLeuGlnValPheLeuGlyValIleAsnThrGluTrpThr 131
        ||||||||||||||||||||||||||||||||||:::
Db 241 TTCCTAGACTACCTGCAAGTATTTCTTGGTCTAATAAACACCGAGTGGAGT 291

RESULT 12
AAA34857
ID AAA34857 standard; DNA; 816 BP.
XX
AC AAA34857;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2546.
XX
CC Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; 88.
XX
OS Homo sapiens.
XX
PN WO20009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX

PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 716; 1343pp; English.
XX

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

US-10-787-382-5 (1-134) x AAA34857 (1-816)

Alignment Scores:
Pred. No.:
Score: 1.23e-44
Percent Similarity: 430.00   Length: 816
Best Local Similarity: 77.61%   Matches: 87
Query Match: 64.93%   Conservative: 17
DB: 61.78%   Mismatches: 30
                       3   Indels: 0
                                     Gaps: 0

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
Db 45 ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC 104

Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
Db 105 CCCAGAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCCTTGGCACTGCTTTCTACTCAT 164

Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db 165 CGAACTCTGCTGATAGGCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAAATCAC 224

Qy 61 GlnLeuCysIleLeuLysGlyValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
Db 225 CAACTGTGCACTGAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTGCAAAACTGCAA 284

Qy 81 GlyGluAlaValAspLysPheGlnAsnLeuSerLeuLeuLysGluHisIleGluArg 100
Db 285 GGGGGTACTGTGGAAAGACTATTCAAAACTTGTCCTTAATAAGAAATACATTGACGGC 344

Qy 101 GlnLysLysArgCysAlaGlyArgTrpArgValThrLysSerPheLeuAspTyrLeuGln 120
Db 345 CAAAAAAAAAGTGTGCGAGAAGAAGACCGGAGAGTAAACCAAATTCCTAGACTACCTGCAA 404

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpProGluSer 134
Db 405 GAGTTCTTGGTGGTAATGAACACCGAGTGGGATAATAGAAAGT 446

Db AAA13338;

RESULT 13

ID AAA13338
AAA13338 standard; cDNA; 816 BP.
XX
AC AAA13338;
XX
DT 25-JUL-2000 (first entry)
XX
OS Homo sapiens.
XX
DE Human interleukin-5 (IL-5) nucleotide sequence.
XX
KW Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;
KW antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;
KW allergic conjunctivitis; inhibitor; ss.
XX
PN US6048726-A.
XX
PD 11-APR-2000.
XX
PF 15-MAY-1998; 98US-00079839.
XX
PR 15-MAY-1998; 98US-00079839.
XX
PA (WELT/) WELTMAN J K.
PA (KARI/) KARIM A S.
XX
PI Weltman JK, Karim AS;
XX
DR WPI; 2000-302784/26.
XX
PT Oligonucleotide comprising non-natural internucleoside linkage, useful
PT for inhibiting interleukin-5 expression and treating inflammatory
PT diseases, asthma, allergic rhinitis, allergic conjunctivitis.
XX
CC Oligonucleotide comprising non-natural internucleoside linkage, useful
CC for inhibiting interleukin-5 expression and treating inflammatory
CC diseases, asthma, allergic rhinitis, allergic conjunctivitis.
CC This sequence represents the human interleukin-5 (IL-5) encoding
CC nucleotide sequence. Interleukin-5 is involved in eosinophilic
CC inflammation and inflammatory disorders. The present invention relates to
CC an IL-5 antisense oligonucleotide (see AAA13337) which inhibits the
CC expression of IL-5. The antisense oligonucleotide has at least one non-
CC natural internucleoside linkage. The oligonucleotide is able to inhibit
CC IL-5 secretion in a dose dependent manner, and is useful for inhibiting
CC IL-5 expression and therefore treating inflammatory diseases, asthma,
CC allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases
CC such as eczema
XX
PS Disclosure; Col 3-4; 11pp; English.
XX
SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

US-10-787-382-5 (1-134) x AAA13338 (1-816)

Alignment Scores:
Pred. No.:
Score: 1.23e-44
Percent Similarity: 430.00   Length: 816
Best Local Similarity: 77.61%   Matches: 87
Query Match: 64.93%   Conservative: 17
DB: 61.78%   Mismatches: 30
                       3   Indels: 0
                                     Gaps: 0

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
Db 45 ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC 104

Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
Db 105 CCCAGAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCCTTGGCACTGCTTTCTACTCAT 164

Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60

```
Db   165  CGAACTCTGGTAGCCAATGAGACTCTGAGGATTCCTCGTTCCTGTACATAAAATCAC
          ||||||                       ::             ||||||||||
Qy    61  GlnLeuCysIleLysGluValPheGlnInGlyIleAspThrLeuLysAsnGlnThrAlaHis  80
          ||||||:::||||||||||||:::||||:::||||:||:||||||||
Db   225  CAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA  284
          ||||||:::||||||||||||:::||||:::||||:||:||||||||
Qy    81  GlyGluAlaValAlaGlyLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
          ||||||||||::::::||||||||||||||:::||||:::|||||
Db   285  GGGGGTGACTGTGGAAAGACTATTCAAAAAACTTGTCCTTAATAAAGAAAATACATTGACGGC  344
          ||||||||||||||::::::|||||||||||::||||:::||||:::
Qy   101  GlnLeuLysArgCysAlaGlyLeuArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
          |||||||||||||:::::||||||::||||||||||||||
Db   345  CAAAAAAAAAGTGTGGAGAAGACGGAGAGTAAACCAATTCCTAGACTTACCTGCAA  404
          ||||||||||||||||:::||||||||||||
Qy   121  ValPheLeuGlyValIleAsnThrGluTrpProGluSer  134
          |||||||||||||||||:::||||||
Db   405  GAGTTTCTTGGTGTTAATGAACACCGGAGTGGATAAATAGAAAGT  446
```

RESULT 14
AAF20979

```
Alignment Scores:
Pred. No.:
Score:                1.23e-44        Length:            816
Percent Similarity:   430.00          Matches:            87
Best Local Similarity: 77.61%         Conservative:       17
Query Match:          64.93%          Mismatches:         30
DB:                   61.78%          Indels:              0
                      3               Gaps:                0
```

US-10-787-382-5 (1-134) x AAF20979 (1-816)

```
Qy     1  MetArgThrLeuIleLeuGlyAspAlaAsnLeuMetIleProThrProGluAsnLeuAsnHis  20
          ||||                        :::             :::
Db     1  ATGAGGATGCTTCTGCATTTGAGTTGCTAGCTCTTGGAGCTGCTGCTGTATGCCATC  60
Qy    21  AlaLeuGluAlaProMetAsnArgLeuValAlaAlaGlyThrLeuThrLeuLeuSerThrHis  40
          :::                         |||||
Db    45  CCCACAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT  164
Qy    41  ArgThrThrLeuIleLeuGlyAspAlaAsnLeuMetIleProThrProGluAsnLeuAsnHis  60
          |||||                   :::             |||||
Db   105  CCGAACTCTGCTGATAGCCAATGAGACTCTGAGGATTCCTCGTTCCTGTACATAAAATCAC  224
Qy    61  GlnLeuCysIleLysGluValPheGlnInGlyIleAspThrLeuLysAsnGlnThrAlaHis  80
          ||||||:::|||||||||:::||||:::||||:||:|||||
Db   165  CAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA  284
Qy    81  GlyGluAlaValAlaGlyLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
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Qy   101  GlnLeuLysArgCysAlaGlyLeuArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
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RESULT 15
ADG33104

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KW   ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW   diverticulitis; primary biliary sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200309694-A2.
XX
PD   06-NOV-2003.
XX
PF   24-APR-2003; 2003WO-US013015.
XX
PR   24-APR-2002; 2002US-00131827.
XX
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI   Wohlgemuth J, Fry K, Woodward R, Ly N;
XX
DR   WPI; 2003-877243/81.
XX
PT   Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT   such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT   colitis, psoriasis and asthma by detecting the expression level of one or
PT   more genes.
XX
PS   Claim 18; SEQ ID NO 428; 877pp; English.
XX
CC   This invention relates to novel methods for diagnosing and monitoring
CC   autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC   the identification of genes that have a clinical utility as diagnostic
CC   tools for the management of, in particular, patients with systemic lupus
CC   erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC   present invention describes a method for determining the levels of
CC   multiple differentially expressed genes of a patient, in a concerted
CC   manner, in order to achieve an improved diagnostic assay with sensitivity
CC   and specificity for the disease in question. As such, these genes are
CC   useful for the diagnosis of various other inflammatory disorders
CC   including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC   ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC   cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC   This polynucleotide is a DNA sequence representing human mRNA that is
CC   differentially expressed in patients with SLE, used in an exemplification
CC   of the invention.
XX
SQ   Sequence 816 BP; 276 A; 137 C; 165 G; 238 T; 0 U; 0 Other;

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Pred. No.:
Score:                  1.23e-44
Percent Similarity:     430.00          Length:         816
Best Local Similarity:  77.61%          Matches:        87
Query Match:            64.93%          Conservative:   17
DB:                     61.78%          Mismatches:     30
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US-10-787-382-5 (1-134) x ADG33104 (1-816)

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Qy      61 GlnLeuCysIleLysGlyValPheGlyGlnLysIleAspThrLeuLysAsnGlnThrAlaHis 80
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Qy      81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
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Qy     101 GlnLysLysArgCysAlaGlyLysGluArgTrpAspValThrLysLysPheLeuAspTyrLeuGln 120
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Qy     121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Search completed: August   6, 2005, 21:26:45
Job time : 375.482 secs
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OM protein - protein search, using sw model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             August  4, 2005, 17:11:16 ; Search time 114.088 Seconds
                                                (without alignments)
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Title:              US-10-787-382-5
Perfect score:      696
Sequence:           1 MRMLLNLSILALGAYVSAF.........FLDYLQVPLGVINTEMTPES 134

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters:      1752860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

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   13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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   20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
   21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	696	100.0	134	9	US-09-755-633-5	Sequence 5, Appli
2	696	100.0	134	14	US-10-218-654-81	Sequence 81, Appl
3	696	100.0	134	14	US-10-262-439-81	Sequence 81, Appl
4	696	100.0	134	16	US-10-787-382-5	Sequence 5, Appli
5	610	87.6	115	9	US-09-755-633-10	Sequence 10, Appl
6	610	87.6	115	14	US-10-218-654-86	Sequence 86, Appl
7	610	87.6	115	14	US-10-262-439-86	Sequence 86, Appl
8	610	87.6	115	16	US-10-787-382-10	Sequence 10, Appl
9	610	87.6	115	16	US-10-289-454-233	Sequence 233, Appl
10	430	61.8	134	14	US-10-400-377-12	Sequence 12, Appl
11	430	61.8	134	14	US-10-400-708-12	Sequence 12, App
12	430	61.8	134	14	US-10-298-148-12	Sequence 12, Appl
13	430	61.8	134	14	US-10-050-902-233	Sequence 233, App
14	430	61.8	134	14	US-10-050-898-233	Sequence 233, Appl
15	430	61.8	134	16	US-10-773-939-12	Sequence 12, Appl
16	430	61.8	134	16	US-10-773-654-12	Sequence 12, Appl
17	430	61.8	134	18	US-10-774-149-12	Sequence 12, Appl
18	430	61.8	134	16	US-10-880-101A-86	Sequence 86, Appl
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23	430	61.8	134	18	US-10-880-101A-92	Sequence 92, Appl
24	430	61.8	134	16	US-10-846-911-9	Sequence 9, Appli
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29	430	61.8	285	14	US-10-846-911-15	Sequence 15, Appl
30	430	59.7	287	14	US-10-846-911-15	Sequence 15, Appl
31	415.5	59.7	287	14	US-10-295-074-15	Sequence 15, Appl
32	415.5	59.7	287	16	US-10-846-911-13	Sequence 13, Appl
33	413.5	59.4	287	14	US-10-295-074-13	Sequence 13, Appl
34	413.5	59.4	287	16	US-10-846-911-13	Sequence 13, Appli
35	359	51.6	136	14	US-10-289-454-336	Sequence 336, App
36	359	51.6	136	14	US-10-050-902-336	Sequence 336, Appl
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43	357	51.3	138	14	US-10-289-454-335	Sequence 335, App
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51	356	51.1	136	14	US-10-295-074-13	Sequence 13, Appli
52	356	51.1	115	16	US-10-658-834A-580	Sequence 580, App
53	356	51.1	115	16	US-10-658-834A-587	Sequence 587, App
54	356	51.1	115	16	US-10-658-834A-589	Sequence 589, App
55	356	51.1	115	16	US-10-658-834A-595	Sequence 595, App
56	356	51.1	115	14	US-10-846-911-1	Sequence 1, Appli
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58	355	51.0	115	16	US-10-658-834A-574	Sequence 574, App
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62	355	51.0	115	16	US-10-658-834A-585	Sequence 585, App
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89	344	49.4	136	14	US-10-050-898-332	Sequence 332, App
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95	343	49.3	121	14	US-10-050-902-334	Sequence 334, App
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97	342	49.1	115	16	US-10-658-83A-601	Sequence 601, App
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99	75.5	10.8	367	15	US-10-264-237-2786	Sequence 2786, A
100	75.5	10.8	490	18	US-10-467-535-8	Sequence 8, Appli

RESULT 1

US-09-755-633-5
; Sequence 5, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR APPLICATION FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR APPLICATION FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-5

Query Match   100.0%;   Score 696;   DB 9;   Length 134;
Best Local Similarity   100.0%;   Pred. No. 1.4e-71;
Matches 134;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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ALIGNMENTS

RESULT 2

US-10-218-654-81
; Sequence 81, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR APPLICATION FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR APPLICATION FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-81

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Matches 134;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy  121  VFLGVINTEWTPES 134
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RESULT 3

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; Sequence 81, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 10/218,654
; PRIOR APPLICATION FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR APPLICATION FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR APPLICATION FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-81

Query Match   100.0%;   Score 696;   DB 14;   Length 134;
Best Local Similarity   100.0%;   Pred. No. 1.4e-71;
Matches 134;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy  121  VFLGVINTEWTPES 134
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Db  121  VFLGVINTEWTPES 134
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Qy   121 VFLGVINTEWTPES 134
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Db   121 VFLGVINTEWTPES 134

RESULT 4
US-10-787-382-5
; Sequence 5, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR APPLICATION NUMBER: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris

Query Match   100.0%; Score 696; DB 16; Length 134;
Best Local Similarity   100.0%;
Matches 134; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRMLINLSLLALGRAYVSAPAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRMLINLSLLALGRAYVSAPAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
          ||||||||||||||
Db   121 VFLGVINTEWTPES 134

RESULT 5
US-09-755-633-10
; Sequence 10, Application US/09755633
; Patent No. US2002012720OA1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris

Query Match   87.6%; Score 610; DB 9; Length 115;
Best Local Similarity   100.0%;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   20 PAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 PAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   80 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

RESULT 6
US-10-218-654-86
; Sequence 86, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris

Query Match   87.6%; Score 610; DB 14; Length 115;
Best Local Similarity   100.0%;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   20 PAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 PAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   80 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

RESULT 7
US-10-262-439-86
; Sequence 86, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-86

Query Match   87.6%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.3e-62;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   20 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   80 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

RESULT 8
US-10-787-382-10
Sequence 10, Application US/10787382
Publication No. US20040191868A1
GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-787-382-10

Query Match   87.6%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 8.3e-62;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   20 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   80 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

RESULT 9
US-10-289-454-233
Sequence 233, Application US/10289454
Publication No. US20030157479A1
GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: precursor human IL-5
US-10-289-454-233

Query Match   61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.8e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNH 60
         |||||:|:|||||||||| |||||||||||||||||||| |: |||| |||||:||||
Db   1 MRMLLHLSLLALGAAYVVALPTEIPTSALVKEFLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
         |||::| ||| :|: |||||||||||||||||||: :||| :|||||||||||:||||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQ 120

Qy 121 VFLGVINTEWTPES 134
         |||||:|||| ||
Db 121 EFLGVMNTEWIIES 134

RESULT 10
US-10-400-377-12
Sequence 12, Application US/10400377
Publication No. US20030162949A1
GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-12

Query Match   61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.8e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNH 60
         |||||:|:|||||||||| |||||||||||||||||||| |: |||| |||||:||||
Db   1 MRMLLHLSLLALGAAYVVALPTEIPTSALVKEFLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
         |||::| ||| :|: |||||||||||||||||||: :||| :|||||||||||:||||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQ 120

Qy 121 VFLGVINTEWTPES 134
         |||||:|||| ||
Db 121 EFLGVMNTEWIIES 134

RESULT 11
US-10-400-708-12
; Sequence 12, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-12

Query Match   61.8%; Score 430; DB 14; Length 134;
Best Local Similarity   64.9%; Pred. No. 4.8e-41;
Matches 87; Conservative 17; Mismatches 30; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
           |||||||:|||||||||||:|:| |:|||||||||||||||||| |:||
Db   1 MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
           |:|:|||||||||||:||:|| |||||||||||||||||| ||||:||:|||||||||
Db   61 QLCTBEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
           |||:||||||| ||
Db   121 EFLGVMNTEWIIES 134

RESULT 12
US-10-298-148-12
; Sequence 12, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-12

Query Match   61.8%; Score 430; DB 14; Length 134;
Best Local Similarity   64.9%; Pred. No. 4.8e-41;
Matches 87; Conservative 17; Mismatches 30; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
           |||||||:|||||||||||:|:| |:|||||||||||||||||| |:||
Db   1 MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
           |:|:|||||||||||:||:|| |||||||||||||||||| ||||:||:|||||||||
Db   61 QLCTBEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
           |||:||||||| ||
Db   121 EFLGVMNTEWIIES 134

RESULT 13
US-10-050-902-233
; Sequence 233, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-233

Query Match   61.8%; Score 430; DB 14; Length 134;
Best Local Similarity   64.9%; Pred. No. 4.8e-41;
Matches 87; Conservative 17; Mismatches 30; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
           |||||||:|||||||||||:|:| |:|||||||||||||||||| |:||
Db   1 MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
           |:|:|||||||||||:||:|| |||||||||||||||||| ||||:||:|||||||||
Db   61 QLCTBEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
           |||:||||||| ||
Db   121 EFLGVMNTEWIIES 134

RESULT 14
US-10-050-898-233
; Sequence 233, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array

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;  FILE REFERENCE: 1700.0190005
;  CURRENT APPLICATION NUMBER: US/10/050,898
;  CURRENT FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/262,379
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: US 60/288,549
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/326,998
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: US 60/331,045
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: Patentin Ver. 2.1
;
;  SEQ ID NO 233
;  LENGTH: 134
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-050-898-233

        Query Match      61.8%;   Score 430;   DB 14;   Length 134;
        Best Local Similarity    64.9%;   Pred. No. 4.8e-41;
        Matches   87;   Conservative  17;   Mismatches  30;   Indels  0;   Gaps  0;

Qy   1  MRMLLNLSLLALGAAAYSAFAVENPMRLVAETLTLLSTHRTWLIGDCNLMIPTPENKNH  60
           |||:||:|:|||||: ||:|||||||||||:: |||||||||||||||| :|||:|
Db   1  MRMLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH  60

Qy  61  QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKRCAGERWRVTKFLDYLQ 120
           ||:||||:|||||||||||||||||||||||||||||||||||||||||||: ||||||
Db  61  QLCTEEIFQGIGTLBSQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy 121  VFLGVINTEWTPES 134
           ||||:||||| ||
Db 121  EFLGVMNTEWIIES 134
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RESULT 15
US-10-773-939-12
;  Sequence 12, Application US/10773939
;  Publication No. US20040175356A1
;  GENERAL INFORMATION:
;  APPLICANT: Cox III, George N
;  APPLICANT: Bolder Biotechnology, Inc.
;  TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
;  FILE REFERENCE: 4152-1-PUS
;  CURRENT APPLICATION NUMBER: US/10/773,939
;  CURRENT FILING DATE: 2004-02-05
;  PRIOR APPLICATION NUMBER: US/10/400,377
;  PRIOR FILING DATE: 2003-03-26
;  PRIOR APPLICATION NUMBER: US/09/462,941
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/052,516
;  PRIOR FILING DATE: 1997-07-14
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: Patentin Ver. 2.0
;
;  SEQ ID NO 12
;  LENGTH: 134
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-773-939-12

        Query Match      61.8%;   Score 430;   DB 16;   Length 134;
        Best Local Similarity    64.9%;   Pred. No. 4.8e-41;
        Matches   87;   Conservative  17;   Mismatches  30;   Indels  0;   Gaps  0;

Qy   1  MRMLLNLSLLALGAAAYSAFAVENPMRLVAETLTLLSTHRTWLIGDCNLMIPTPENKNH  60
           |||:|||:|:|||||: ||:|||||||||||:: ||||||||||||| :|||:|
Db   1  MRMLLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH  60

Qy  61  QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKRCAGERWRVTKFLDYLQ 120
           ||:||||:|||||||||||||||||||||||||||||||||||||||||||: ||||||
Db  61  QLCTEEIFQGIGTLBSQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120
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Qy 121  VFLGVINTEWTPES 134
           ||||:||||| ||
Db 121  EFLGVMNTEWIIES 134

Search completed: August   4, 2005, 17:30:11
Job time : 116.088 secs
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: August 4, 2005, 16:50:05 ; Search time 134.538 Seconds
(without alignments)
385.213 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLLNLSLLALGAAVSAF............PLDYLQVPLGVINTEWTPES 134

Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :   A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	696	100.0	134	3	AAY58219	Aay58219 Canine in
2	687	98.7	134	4	AAB72615	Aab72615 Canine in
3	610	87.6	115	3	AAY58220	Aay58220 Canine ma
4	536	77.0	132	2	AAW08479	Aaw08479 Ovine Il-
5	430	61.8	134	2	AAR92802	Aar92802 Human int
6	430	61.8	134	4	AAB72617	Aab72617 Human int
7	430	61.8	134	5	ABG94294	Abg94294 Human int
8	430	61.8	134	5	ABG80606	Abg80606 Human pre
9	430	61.8	134	5	AAU10353	Aau10353 Interleuk
10	430	61.8	134	7	ADF70849	Adf70849 Human int
11	430	61.8	134	7	ADK17207	Adk17207 Human int
12	430	61.8	134	6	ADP56010	Adp56010 Human PRO
13	430	61.8	285	6	AAO30457	Aao30457 hIL5-P30-
14	430	61.6	285	6	AAO30458	Aao30458 hIL5-P2-P
15	429	61.6	84	4	AAB72616	Aab72616 Canine in
16	426	60.3	134	5	AAU10354	Aau10354 Interleuk
17	420	60.3	134	6	AAP81056	Aap81056 Sequence
18	415.5	59.7	287	6	AAO30460	Aao30460 hIL5.37 v
19	413.5	59.4	287	6	AAO30459	Aao30459 hIL5.36 v
20	376	54.0	133	1	AAP71064	Aap71064 Murine eo
21	376	54.0	133	2	AAR96963	Aar96963 T cell re
22	376	54.0	133	2	AAW72949	Aaw72949 T cell re
23	376	54.0	133	2	AAW72947	Aaw72947 T cell re
24	376	54.0	133	4	AAB72618	Aab72618 Murine in
25	375	53.9	133	1	AAP82969	Aap82969 B cell di
26	359	51.6	136	5	ABG94352	Abg94352 Human C-I
27	359	51.6	136	5	ABG80664	Abg80664 Human IIn
28	359	51.6	136	7	ADK17223	Adk17223 Human C-I
29	358	51.4	113	1	ADL89254	Adl89254 Human mod
30	357	51.3	113	1	AAP93152	Aap93152 Sequence
31	357	51.3	138	7	ADK17222	Adk17222 Human C-I
32	357	51.3	123	5	ABG94353	Abg94353 Human C-I
33	357	51.3	123	5	ABG80665	Abg80665 Human IL-
34	357	51.3	123	7	ADK17224	Adk17224 Human C-I
35	357	51.3	138	5	ABG94351	Abg94351 Human C-I
36	356	51.1	138	5	ABG80663	Abg80663 Human IIn
37	356	51.1	115	5	AAB45489	Aab45489 Human int
38	356	51.1	112	7	ADK17208	Adk17208 Human C-I
39	356	51.1	115	5	ABG94295	Abg94295 Human mat
40	356	51.1	115	5	ABG80607	Abg80607 Human int
41	356	51.1	115	6	AAO30453	Aao30453 Human int
42	356	51.1	115	7	AAP80279	Aap80279 Pleiotrop
43	356	51.1	115	5	AAP81038	Aap81038 Sequence
44	356	51.1	115	6	ADL89253	Adl89253 Human mod
45	356	51.1	115	8	ADL89261	Adl89261 Human mod
46	356	51.1	115	8	ADL89262	Adl89262 Human mod
47	356	51.1	115	8	ADL89243	Adl89243 Human mod
48	356	51.1	115	8	ADL88874	Adl88874 Human cyt
49	356	51.1	115	8	ADL89240	Adl89240 Human mod
50	356	51.1	115	8	ADL89246	Adl89246 Human mod
51	355	51.0	115	8	ADL89255	Adl89255 Human mod
52	355	51.0	115	8	ADL89251	Adl89251 Human mod
53	355	51.0	115	8	ADL89256	Adl89256 Human mod
54	355	51.0	115	8	ADL89247	Adl89247 Human mod
55	355	51.0	115	8	ADL89264	Adl89264 Human mod
56	355	51.0	133	1	ADL89234	Adl89234 Human mod
57	355	51.0	115	8	ADL89260	Adl89260 Human mod
58	354	50.9	115	8	ADL89241	Adl89241 Human mod
59	354	50.9	115	8	ADL89263	Adl89263 Human mod
60	354	50.9	115	8	ADL89244	Adl89244 Human mod
61	353	50.7	115	8	ADL89245	Adl89245 Human mod
62	353	50.7	115	8	ADL89259	Adl89259 Human mod
63	353	50.7	115	8	ADL89250	Adl89250 Human mod
64	352	50.6	115	8	ADL89239	Adl89239 Human mod
65	352	50.6	115	8	ADL89238	Adl89238 Human mod
66	352	50.6	115	8	ADL89249	Adl89249 Human mod
67	351	50.4	115	8	ADL89258	Adl89258 Human mod
68	351	50.4	115	8	ADL89265	Adl89265 Human mod
69	351	50.4	115	8	ADL89257	Adl89257 Human mod
70	351	50.4	115	8	ADL89266	Adl89266 Human mod
71	351	50.4	115	8	ADL89248	Adl89248 Human mod
72	351	50.4	115	8	ADL89252	Adl89252 Human mod
73	351	50.4	115	8	ADL89236	Adl89236 Human mod
74	351	50.4	115	8	ADL89237	Adl89237 Human mod
75	351	50.4	121	2	AAP80280	Aap80280 Murine pl
76	351	50.4	121	2	AAW43436	Aaw43436 Murine mod
77	350	50.0	115	8	ADL89242	Adl89242 Human mod
78	350	50.0	115	2	AAW05273	Aaw05273 N-termina
79	347	49.9	115	2	AAW72948	Aaw72948 Truncated
80	347	49.9	134	5	ABG94349	Abg94349 Human C-I
81	347	49.9	134	5	ABG80661	Abg80661 Human IL-
82	347	49.9	134	7	ADK17220	Adk17220 Mouse C-I
83	347	49.9	134	7	ADK17209	Adk17209 Mouse int
84	344	49.4	136	5	ABG94350	Abg94350 Mouse C-I
85	344	49.4	136	5	ABG80662	Abg80662 Mouse IL-
86	344	49.4	136	5	ABG80660	Abg80660 Mouse IL-
87	343	49.3	113	2	AAW05274	Aaw05274 N-termina
88	343	49.3	113	5	ABG94348	Abg94348 Mouse IL-
89	343	49.3	113	7	ADK17219	Adk17219 Mouse C-I
90	343	49.3	134	7	ADK17221	Adk17221 Mouse C-I
91	343	49.3	115	8	ADL89268	Adl89268 Human mod
92	343	49.3	121	5	ABG94296	Abg94296 Mouse Int
93	343	49.3	121	5	ABG80608	Abg80608 Mouse mat
94	343	49.3	121	7	ADK17209	Adk17209 Mouse int
95	342	49.1	112	2	AAW05275	Aaw05275 N-termina
96	342	49.1	115	7	ADL89267	Adl89267 Human mod
97	339	48.7	126	3	AAB45494	Aab45494 Modified
98	335	48.1	132	3	AAB45498	Aab45498 Modified

RESULT 1

AAY58219						
99	332.5	47.8	126	3	AAB45490	Aab45490 Modified
100	332.5	47.8	126	3	AAB45514	Aab45514 Modified

ALIGNMENTS

```
ID   AAY58219 standard; protein; 134 AA.
XX
AC   AAY58219;
XX
DT   14-MAR-2000  (first entry)
XX
DE   Canine interleukin-5 (IL-5).
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS   Canis familiaris.
XX
PN   WO961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 3h; Page 224; 264pp; English.
XX
CC   Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
CC   -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3
CC   ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
CC   canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
CC   granulocyte macrophage colony-stimulating factor (GMCSF), and nucleotides
CC   which encode these immunoregulatory proteins. The proteins, their
CC   associated nucleic acid, specific antibodies and inhibitors may be used
CC   as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   of activity, while the antibodies may be used in detection, and in drug
CC   targetting
XX
SQ   Sequence 134 AA;

Query Match             100.0%;  Score 696; DB 3;  Length 134;
Best Local Similarity   100.0%;
Matches  134;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60

Qy         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120

Qy        121 VFLGVINTEWTPES 134
              ||||||||||||||
Db        121 VFLGVINTEWTPES 134
```

RESULT 2

```
ID   AAB72615 standard; protein; 134 AA.
XX
AC   AAB72615;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Canine interleukin-5 protein #1.
XX
KW   Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW   inflammatory reaction.
XX
OS   Canis sp.
XX
PN   WO200111049-A2.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000;   2000WO-US021651.
XX
PR   10-AUG-1999;   99US-00371615.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Guo H, Lawton R, Mermer B, Alyappa AP;
XX
PT   Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT   generating antibodies which are useful in treating allergies in dogs.
XX
PS   Claim 29; Page 46-47; 48pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC   cancer and inflammatory reactions in dogs. The present sequence is one
CC   version of the IL-5 protein shown in the specification
XX
SQ   Sequence 134 AA;

Query Match             98.7%;  Score 687; DB 4;  Length 134;
Best Local Similarity   99.3%;
Matches  133;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy          1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60

Qy         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120

Qy        121 VFLGVINTEWTPES 134
              |||||||||||| ||
Db        121 VFLGVINTEWTMES 134
```

RESULT 3

```
ID   AAY58220 standard; protein; 115 AA.
XX
AC   AAY58220;
XX
DT   14-MAR-2000  (first entry)
```

XX
DE Canine mature interleukin-5 (IL-5).
XX
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011942.
XX
PR 29-MAY-1998; 98US-0087306P.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
PS Claim 3h; Page 227; 264pp; English.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX
DR WPI; 2000-072623/06.
DR N-PSDB; AAZ55550, AAZ55551.
XX
CC Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
CC -5 (IL-5). The invention relates to canine IL-4, canine or feline interleukin
CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
CC canine IL-5, canine or feline interferon-alpha (IFN-alpha) and feline
CC granulocyte macrophage colony-stimulating factor (GMCSF), and nucleotides
CC which encode these immunoregulatory proteins. The proteins, their
CC associated nucleic acids, specific antibodies and inhibitors may be used
CC as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat immune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g. antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targeting.
XX
SQ Sequence 115 AA;

RESULT 4
AAW08479
ID AAW08479 standard; protein; 132 AA.
XX
AC AAW08479;
XX
DT 17-OCT-2003 (revised)
DT 24-SEP-1997 (first entry)
XX
DE Ovine IL-5.

Query Match   87.6%; Score 610; DB 3; Length 115;
Best Local Similarity   100.0%;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   20  FAVENPMNRLVAEFTLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA   79
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  FAVENPMNRLVAEFTLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA   60

Qy   80  HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES  134
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES  115
```

KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW immunosuppression; allergy; reproductive system; growth; early maturity;
KW antibody; diagnosis; immunopotentiator;
KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon.
XX
OS Ovis aries.
XX
PN WO9700321-A1.
XX
PD 03-JAN-1997.
XX
PF 14-JUN-1996; 96WO-AU000360.
XX
PR 14-JUN-1995; 95AU-00003502.
PR 27-OCT-1995; 95AU-0006244.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Seow H, Wood P;
XX
PS Claim 31; Page 39-40; 78pp; English.
XX
PT Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT adjuvants and to treat or prevent microbial infections in livestock.
XX
DR WPI; 1997-077528/07.
DR N-PSDB; AAT50755, AAT50756.
XX
CC This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5
CC or IL-12 are used to treat and/or prevent infections in livestock (esp.
CC cows and sheep), particularly where the animals are stressed, e.g. during
CC transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for
CC veterinary use (partic. weakly immunogenic subunit or synthetic peptide
CC vaccines). They may also be used to treat cancer, immunosuppression and
CC allergy, to enhance/suppress the reproductive system and to promote
CC growth or early maturity. Optionally interleukin can be delivered from
CC constructs or delivery cells and antibodies are useful in enzyme
CC immunoassays for rapid diagnosis of infection. The interleukins are
CC immunopotentiators, especially IL-5 promotes growth of early
CC haematopoietic progenitor cells and generation of cytotoxic cells from
CC thymocytes, also it stimulates production and secretion of IgM and IgA
CC (in synergism with bacterial endotoxin). IL-12 induces production of
CC gamma-interferon by, and proliferation of, T and NK cells and increases
CC the (non-)specific cytolytic lymphocyte response. The genetic constructs
CC can also be used for in vitro production of IL-5 or -12. (Updated on 17-
CC OCT-2003 to standardise OS field)
XX
SQ Sequence 132 AA;

RESULT 5
AAR92802
ID AAR92802 standard; protein; 134 AA.
XX
AC AAR92802;

Query Match   77.0%; Score 536; DB 2; Length 132;
Best Local Similarity   78.8%;
Matches 104; Conservative   15; Mismatches   13; Indels   0; Gaps   0;

```
Qy    3  MLINLSLIALGAAYSAFAVENPMNRLVAEFTLTLLSTHRTWLIGDGNLMIPTPENKNHQL   62
         |||| :|| :|||| ||: ||||||||||||||||||||||||||||||||||::||||||
Db    1  MHLRLTLVAILGAAYVCANAVESTMNRLVAEFTLTLLSTHQTLLIGDGNLMIPTPQHTNHQL   62

Qy   63  CIKEVPQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVF  122
         |||:|:||||||||||::|:||: |:|||||||||||:|:||: |: |:||||||||||
Db   61  CIEEVFQGIDTLKNQTAQGDAVKKIFRNLSLIKEYIDLQKRKCGGERWRVKQFLDYLQVF  120

Qy  123  LGVINTEWTPES  134
         ||||||||||||
Db  121  LGVINTEWTMS  132
```

XX
DT   24-MAY-1996   (first entry)
XX
DE   Human interleukin-5.
XX
KW   Cytokine; mutein; interleukin-5; agonist; antagonist; diagnosis; therapy;
KW   cancer; inflammation; degenerative disease.
XX
OS   Homo sapiens.
XX
PN   WO960430-A2.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-US008950.
XX
PR   01-AUG-1994;   94US-0028439.
XX
PA   (SCHE) SCHERING CORP.
XX
PI   Zurawski SM, Zurawski G;
XX
DR   WPI; 1996-129335/13.
XX
SQ   Sequence 134 AA;

PS   Disclosure; Page 43; 52pp; English.
XX
PT   Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and murine
PT   P600 contg. amino acid substitutions. - useful for the diagnosis and
PT   treatment of cancer, inflammation, etc.
XX
CC   Muteins of human interleukin-5 (AAR928802) and other cytokines (see also
CC   AAR92790-801) are obtd. by site-directed mutagenesis of natural cytokine
CC   are useful in the screening of cytokine and cytokine receptor levels, and
CC   at positions identified as critical for activity. The muteins
CC   in the diagnosis or treatment of e.g. inflammation, cancer, and
CC   degenerative disorders
XX
SQ   Sequence 134 AA;

Query Match   61.8%;   Score 430;   DB 2;   Length 134;
Best Local Similarity   64.9%;   Pred. No. 6.8e-43;
Matches   87;   Conservative   17;   Mismatches   30;   Indels   0;   Gaps   0;

```
Qy    1 MRMLLNLSLLALGAAYVSAFAPAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
        |||||:|||||||||:||:::||||||:|||||:|||:|||||||:::||||:|:::|||
Db    1 MRMLLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGREAVDKLFQNLSLIKEHIERQKRCAGRWRVTKFLDYLQ 120
        |||:::|:|||||:::|:|::|||:|||||||||||:::|||||||||||||||||||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy  121 VFLGVINTEWTPES 134
        :|||:|:||| ||
Db  121 EFLGVMNTEWIIES 134
```

RESULT 6
AAB72617
ID   AAB72617 standard; protein; 134 AA.
XX
AC   AAB72617;
XX
DT   04-MAY-2001   (first entry)
XX
DE   Human interleukin-5.
XX
KW   Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW   inflammatory reaction; human.
XX
OS   Homo sapiens.
XX
PN   WO20011049-A2.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000;   2000WO-US021651.
XX
PR   10-AUG-1999;   99US-00371615.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Guo H, Lawton R, Mermer B, Alyappa AP;
XX
DR   WPI; 2001-191542/19.
XX
SQ   Sequence 134 AA;

PS   Disclosure; Fig 2; 48pp; English.
XX
PT   Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT   generating antibodies which are useful in treating allergies in dogs.
XX
CC   The present invention provides the protein and coding sequences of the
CC   canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC   cancer and inflammatory reactions in dogs. The present sequence is human
CC   IL-5
XX
SQ   Sequence 134 AA;

Query Match   61.8%;   Score 430;   DB 4;   Length 134;
Best Local Similarity   64.9%;   Pred. No. 6.8e-43;
Matches   87;   Conservative   17;   Mismatches   30;   Indels   0;   Gaps   0;

```
Qy    1 MRMLLNLSLLALGAAYVSAFAPAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
        |||||:|||||||||:||:::||||||:|||||:|||:|||||||:::||||:|:::|||
Db    1 MRMLLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGREAVDKLFQNLSLIKEHIERQKRCAGRWRVTKFLDYLQ 120
        |||:::|:|||||:::|:|::|||:|||||||||||:::|||||||||||||||||||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy  121 VFLGVINTEWTPES 134
        :|||:|:||| ||
Db  121 EFLGVMNTEWIIES 134
```

RESULT 7
ABG94294
ID   ABG94294 standard; protein; 134 AA.
XX
AC   ABG94294;
XX
DT   10-DEC-2002   (first entry)
XX
DE   Human interleukin 5 precursor protein.
XX
KW   Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW   cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW   vaccine; infectious disease.
XX
OS   Homo sapiens.
XX
PN   WO200256905-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002;   2002WO-IB000166.
XX
PR   19-JAN-2001;   2001US-0262379P.
PR   04-MAY-2001;   2001US-0288549P.
PR   05-OCT-2001;   2001US-0269998P.
PR   07-NOV-2001;   2001US-0331045P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P,
PI   Plossek C;
XX

DR   WPI; 2002-627351/67.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PS   diseases.
XX
XX   Disclosure; Page 422; 441pp; English.
XX
CC   This invention relates to a novel ordered and repetitive antigen array
CC   used in the production of vaccines for infectious diseases. The invention
CC   also discloses a composition comprising a non-natural molecular scaffold
CC   comprising a core particle selected from a core particle of a non-natural
CC   origin and a core particle of natural origin and an organiser comprising
CC   at least one first attachment site, where the organiser is connected to
CC   the core particle by at least one covalent bond. Also disclosed is an
CC   antigen or antigenic determinant with at least one second attachment
CC   site, where the antigen or antigenic determinant is amyloid beta peptide
CC   (Abeta1-42) or its fragment and where the second attachment site is
CC   selected from an attachment site and an attachment site not naturally
CC   or antigenic determinant, where the second attachment site is
CC   the antigen or antigenic determinant, where the second attachment site is
CC   capable of association through at least one non-peptide bond to the first
CC   attachment site and where the antigen or antigenic determinant and the
CC   scaffold interact through the association to form an ordered and
CC   repetitive antigen array. The invention also comprises a capsid which
CC   capable of forming a capsid which comprises mutant Qbeta coat protein
CC   having an amino acid sequence selected from five amino acid sequences
CC   fully defined in the specification. The compounds of the invention may
CC   have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC   antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC   immunisation and as a vaccine. The present sequence represents a protein
CC   sequence used to create the compositions of the invention
XX
SQ   Sequence 134 AA;

Query Match   61.8%;   Score 430;   DB 5;   Length 134;
Best Local Similarity 64.9%;   Pred. No. 6.8e-43;
Matches   87;   Conservative   17;   Mismatches   30;   Indels   0;   Gaps   0;

```
Qy    1 MRMLINLSLLALGAAYVSAPAVENPMNRLJVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          || | ||:|||||||| | |:|| |:| :||||||||||||:|||||||| |:|||
Db    1 MRMLLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTPAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFPLDYLQ 120
          | :|:|||:|||||||:|| || ||||||||:| |||||||||||||
Db   61 QLCTEEIFQGIGTLBSQTVQGGTVERLFQNLSLIKKYIDGQKKCCGEERRRVNQFLDYLQ 120

Qy  121 VFLGVINTEWTPES 134
          |||:|||:|||| ||
Db  121 EFLGVMNTEWIES 134
```

RESULT 8
ABG80606
ID   ABG80606 standard; protein; 134 AA.
XX
AC   ABG80606;
XX
DT   29-NOV-2002 (first entry)
XX
DE   Human precursor Interleukin 5.
XX
KW   molecular antigen array; vaccine; antigen; antimicrobial;
KW   molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW   graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW   adult respiratory distress syndrome; ARDS; Crohn's disease;
KW   allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW   Grave's disease; systemic lupus erythematosus; osteoporosis; multiple sclerosis;
KW   inflammatory immune disease; myasthenia gravis;
KW   immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW   angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW   rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW   enterokinase; cysteine-containing linker.
XX

OS   Homo sapiens.
XX
PN   WO20025907-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000168.
XX
PR   19-JAN-2001; 2001US-0262379P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-03269998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (NOVS) NOVARTIS PHARMA AG.
PA   (MAUR/) MAURER P.
PA   (LECH/) LECHNER F.
PA   (ORTM/) ORTMANN R.
PA   (LUEO/) LUEOEND R.
PA   (STAU/) STAUFENBIEL M.
PA   (FREY/) FREY P.
XX
PS   Maurer P, Lechner F, Lueoend R, Staufenbiel M, Frey P;
PI   Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR   WPI; 2002-636514/68.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PS   diseases.
XX
XX   Disclosure; Page 399; 418pp; English.
XX
CC   The invention relates to a composition comprising: (a) a non-natural
CC   molecular scaffold comprising: (i) a core particle selected from: (1) a
CC   core particle of a non-natural origin; and (2) a core particle of natural
CC   origin; and (ii) an organiser comprising at least one first attachment
CC   site, where the organiser is connected to the core particle by at least
CC   one covalent bond; (b) an antigen or antigenic determinant with at least
CC   one second attachment site, where the antigen or antigenic determinant is
CC   amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC   attachment site is selected from: (i) an attachment site not naturally
CC   occurring with the antigen or antigenic determinant; and (ii) an
CC   attachment site naturally occurring with the antigen or antigenic
CC   determinant, where the second attachment site is capable of association
CC   through at least one non-peptide bond to the first attachment site; and
CC   where the antigen or antigenic determinant and the scaffold interact
CC   through the association to form an ordered and repetitive antigen array.
CC   Also included is a process for producing a non-naturally occurring
CC   ordered and repetitive antigen array. The composition is used in
CC   immunisation and as a vaccine for diseases such as influenza, graft
CC   versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC   respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC   acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC   systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC   gravis, immunoproliferative disease lymphadenopathy,
CC   angioimmunoproliferative lymphadenopathy, immunoblastive lymphadenopathy,
CC   rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC   osteoporosis and infectious diseases. The present sequence is an antigen
CC   for use in the array of the invention. The antigen is modified to possess
CC   a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC   or C-terminal linker peptide which serves as the attachment point to a
CC   virus like particle or bacterial protein (the scaffold protein)
XX
SQ   Sequence 134 AA;

Query Match   61.8%;   Score 430;   DB 5;   Length 134;
Best Local Similarity 64.9%;   Pred. No. 6.8e-43;
Matches   87;   Conservative   17;   Mismatches   30;   Indels   0;   Gaps   0;

```
Qy    1 MRMLINLSLLALGAAYVSAPAVENPMNRLJVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          || | ||:|||||||| | |:|| |:| :||||||||||||:|||||||| |:|||
Db    1 MRMLLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60
```

```
Qy      61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERRWRVTKFLDYLQ 120
           ||| :|:|||| |||:||| ||||||| | |:||:||||||||:| :||| |:|||||||||
Db      61 QLCTEEIFQGIGTLESQTVQGGTVERLFQNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy     121 VFLGVINTEWTPES 134
           |||||:||| ||
Db     121 EFLGVMNTEWIIES 134


RESULT 9
AAU10353
ID   AAU10353 standard; protein; 134 AA.
XX
AC   AAU10353;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Interleukin 5 (IL5).
XX
KW   Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;
KW   haplotyping; inflammatory disorder.
XX
OS   Homo sapiens.
XX
XX
PN   WO20177132-A2.
XX
PD   18-OCT-2001.
XX
PF   11-APR-2000; 2000US-0196250P.
XX
PR   11-APR-2001; 2001WO-US012011.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Benivegna SC, Chew A, Choi JY, Denton RR, Kazemi A,
PI   Nandabalan K, Parks KB;
XX
DR   WPI; 2002-041289/05.
DR   N-PSDB; AAS15002.
XX
PT   New haplotypes of the human interleukin 5 gene, useful to diagnose and
PT   treat diseases associated with the gene including inflammatory disorders
PT   such as asthma.
XX
PS   Claim 27; Fig 3; 65pp; English.
XX
CC   The invention relates to haplotyping the human interleukin 5 (IL5) gene
CC   of an individual, comprising determining if the individual has one of the
CC   IL5 haplotypes or haplotype pairs fully defined in the specification.
CC   Haplotyping the IL5 gene of an individual, comprises determining the
CC   identity of the nucleotide at two or more polymorphic sites in one copy
CC   of the gene. The method also involves identifying an association between
CC   a trait and a haplotype or haplotype pair of the IL5 gene, comprising
CC   comparing the frequency of the haplotype/pair in a population exhibiting
CC   the trait with that of a reference population. A higher frequency in the
CC   trait population indicates the trait is associated with the haplotype.
CC   The polynucleotides and screened compounds are useful to develop
CC   treatment for diseases associated with IL-5 activity including
CC   inflammatory disorders such as asthma. The present sequence represents
CC   the amino acid sequence of interleukin 5 (IL5) as described in the method
CC   of the invention
XX
SQ   Sequence 134 AA;

Query Match             61.8%;  Score 430;  DB 5;  Length 134;
Best Local Similarity   64.9%;  Pred. No. 6.8e-43;
Matches    87;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      1 MRMLLNLSLLALGAAYVSAFAVENPMNRLLVAETLTLLSTHRTWLLGDSNLMIPTPENKNH 60
          ||||:|||||||| |||||||:||: |||| ::  ::|: |:|: | .|:.|||::|:
Db      1 MRMLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy     61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERRWRVTKFLDYLQ 120
```

```
Db      61 QLCTEEIFQGIGTLESQTVQGGTVERLFQNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120.
              ||| :|:|||| |||:||| ||||||| | |:||:||||||||:| :||| |:|||||||||

Qy     121 VFLGVINTEWTPES 134
           |||||:||| ||
Db     121 EFLGVMNTEWIIES 134


RESULT 10
ADF70849
ID   ADF70849 standard; protein; 134 AA.
XX
AC   ADF70849;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human interleukin 5 (IL-5).
XX
KW   interleukin 5; IL-5.
KW   aplastic anaemia; acute leukaemia; human; growth hormone super family;
KW   anaemia; neonatal septicaemia; severe chronic neutropenia;
KW   bone marrow transplantation; HIV infection; burn; surgery; dilatation;
KW   GM-CSF; neutropenia; myelosuppressive chemotherapy;
KW   immunostimulant; granulocyte macrophage colony stimulating factor;
XX
OS   Homo sapiens.
XX
PN   US2003171284-A1.
XX
PD   11-SEP-2003.
XX
PF   15-NOV-2002; 2002US-00298148.
XX
PR   11-OCT-2002; 2002US-0418040P.
PR   15-NOV-2001; 2001US-03322285P.
PR   14-JAN-2000; 2000US-00462941.
PR   13-JUL-1998; 98WO-US014497.
PR   14-JUL-1997; 97US-0052516P.
XX
PS   Example 11; SEQ ID NO 12; 56pp; English.
XX
PI   Cox GN, Doherty DH;
XX
PA   (COXG/) COX G N.
PA   (DOHE/) DOHERTY D H.
XX
DR   WPI; 2003-898295/82.
XX
PT   Protecting an animal from a disease or condition, useful for treating
PT   neutropenia, comprises administering to an animal having the disease or
PT   condition a composition comprising GM-CSF cysteine mutein.
XX
CC   The invention describes protecting an animal from a disease or condition
CC   that can be treated by wild-type granulocyte macrophage colony
CC   stimulating factor (GM-CSF) comprising administering to an animal having
CC   the disease or condition a composition comprising GM-CSF cysteine mutein.
CC   The methods are useful for preventing or treating the occurrence of
CC   neutropenia in an animal, the neutropenia is selected from neutropenia
CC   resulting from myelosuppressive chemotherapy, neutropenia associated with
CC   bone marrow transplantation, neutropenia associated with infection with
CC   the human immunodeficiency virus, neutropenia associated with burns,
CC   surgery, dilatation, anaemia and neonatal septicaemia, severe chronic
CC   neutropenia, neutropenia associated with aplastic anaemia and acute
CC   leukaemia. This is the amino acid sequence of human interleukin 5 (IL-5),
CC   a member of the growth hormone super family which also includes GM-CSF.
XX
SQ   Sequence 134 AA;

Query Match             61.8%;  Score 430;  DB 7;  Length 134;
Best Local Similarity   64.9%;  Pred. No. 6.8e-43;
Matches    87;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      1 MRMLLNLSLLALGAAYVSAFAVENPMNRLLVAETLTLLSTHRTWLLGDSNLMIPTPENKNH 60
```

RESULT 11

Db	1 MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60
Qy	1 MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60
Db	61 QLCIKEVFQGIDTLRNQTAHGBAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
Qy	61 QLCIKEVFQGIDTLRNQTAHGBAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
Db	61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKXKCGBEERRRVNQFLDYLQ 120
Qy	121 VFLGVINTEWTPES 134
Db	121 EFLGVWNTEWIES 134

ID ADK17207 standard; protein; 134 AA.
AC ADK17207;
DT 06-MAY-2004 (first entry)
DE Human interleukin-5 precursor for repetitive antigen array.
KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
KW interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
OS Homo sapiens.
PN WO200304164-A2.
PD 15-MAY-2003.
PF 07-NOV-2002; 2002WO-EP012455.
PR 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-0050902.
PR 21-JAN-2002; 2002WO-IB000166.
PR 19-JUL-2002; 2002US-0396636P.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Bachmann M, Jennings G, Sonderegger I;
DR WPI; 2003-441518/41.
PS Disclosure; SEQ ID NO 233; 245pp; English.

The invention relates to a composition comprising a virus-like particle
and at least one antigen, which is a protein or peptide of interleukin
(IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
core particle with at least one first attachment site and at least one
antigen with at least one second attachment site, where the antigen is a
protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
is an attachment site naturally or not naturally occurring with the
antigen or antigenic determinant. The second attachment site is capable
of association to the first attachment site, and where the antigen or
antigenic determinant and the core particle interact through the
association to form an ordered and repetitive antigen array. The
compositions are useful as medicaments, or for manufacturing a medicament
or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
Hodgkin's lymphoma and related diseases. This sequence is used to
generate the compound of the invention.

Composition comprising an ordered and repetitive antigen or antigenic
determinant array, useful as a medicament, or for manufacturing a
medicament for treating allergic eosinophilic diseases, e.g. asthma, or
Hodgkin's lymphoma.

Query Match   61.8%; Score 430; DB 7; Length 134;
Best Local Similarity 64.9%; Pred. No. 6.8e-43;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

SQ Sequence 134 AA;

RESULT 12

Qy	1 MRMLLNLSLLALGAAYVSAFAVENEPMNRLVAETLTLLSTHRTWLLIGDNGLMIPTPENKNH 60
Db	1 MRMLLHLSLLALGAAYVYAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60
Qy	61 QLCIKEVFQGIDTLKNQTAHGBAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
Db	61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKXKCGBEERRRVNQFLDYLQ 120
Qy	121 VFLGVINTEWTPES 134
Db	121 EFLGVWNTEWIES 134

ID ADP56010 standard; protein; 134 AA.
AC ADP56010;
DT 18-NOV-2004 (first entry)
DE Human PRO protein sequence SEQ ID NO:1986.
KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy.
OS Homo sapiens.
PN WO200403956-A2.
PD 13-MAY-2004.
PF 28-OCT-2003; 2003WO-US034381.
PR 29-OCT-2002; 2002US-0422472P.
PA (GENH-) GENENTECH INC.
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
DR WPI; 2004-376182/35.
DR N-PSDB; ADP56009.
PS Claim 1; SEQ ID NO 1986; 3009pp; English.

New PRO polynucleotides and polypeptides, useful in diagnosing
and treating an immune related disease, e.g. systemic lupus
erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
stimulating an immune response.

The present invention describes an isolated PRO nucleic acid (I). Also
described: (1) a vector comprising (II); (2) a host cell comprising the
vector of (1); (3) a process for producing a PRO polypeptide; (4) an
isolated PRO polypeptide; (5) a chimeric molecule comprising the
polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
antibody which specifically binds to a polypeptide of (4); (7) a
composition of matter comprising a polypeptide of (4), an agonist or
antagonist of the polypeptide or an antibody that binds to the
polypeptide in combination with a carrier; (8) an article of manufacture
comprising a container, a label on the container and a composition of
matter of (7); (9) a method of treating an immune related disease in a
mammal; (10) a method for determining the presence of a PRO polypeptide
in a sample suspected of having the polypeptide; (11) a method of
diagnosing an immune related disease or an inflammatory immune response
in mammal; (12) a method of identifying a compound that inhibits or
mimics the activity of or expression of a gene encoding a PRO polypeptide

CC   ; and (13) a method of stimulating the immune response in a mammal. The
CC   PRO sequences have antiallergic, antianaemic, antiarthritic,
CC   antiasthmatic, antidiabetic, antidiarrhoeal,
CC   antirheumatic, antithyroid, antiinflammatory, antipsoriatic,
CC   haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC   nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC   virucide activities, and can be used in gene therapy. The nucleic acid
CC   (I) and the encoded polypeptides, compositions, kits and methods are
CC   useful in diagnosing and treating an immune related disease and in
CC   stimulating an immune response. The present sequence represents a human
CC   PRO protein from the present invention.
XX
SQ   Sequence 134 AA;

Query Match   61.8%; Score 430; DB 8; Length 134;
Best Local Similarity   64.9%; Pred. No. 6.8e-43;
Matches   87; Conservative 17; Mismatches 30; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||| : |||
Db   1 MRMLLHLSLLALGAAYVAVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
              |||:|||:||||:||||||| : ||||| |:||:|||||||| ||||||||| :|||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
              |||||:||||||||
Db   121 BFLGVMNTEWIIES 134

RESULT 13
ID   AAO30457
AC   AAO30457;
XX
DT   22-SEP-2003 (first entry)
XX
DE   hIL5-P30-P2-hIL5 (hIL5.34) fusion construct protein.
XX
KW   Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW   tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
KW   IL5; epitope; human; tetanus toxoid; chimeric.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
FH
FT   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /note= "Human IL5 leader peptide"
FT   Protein   20. .285
FT   /note= "Mature hIL5.34 protein"
XX
PN   WO2003042244-A2.
XX
PD   22-MAY-2003.
XX
PF   15-NOV-2002; 2002WO-DK000764.
XX
PR   16-NOV-2001; 2001DK-00001702.
PR   16-NOV-2001; 2001US-0331575P.
XX
PA   (PHAR-) PHARMEXA AS.
PA   (KLYS/) KLYSNER S.
PA   (NIEL/) NIELSEN F S.
PA   (BRAT/) BRATT T.
PA   (VOLD/) VOLDBORG B.
PA   (MOUR/) MOURITSEN S.
XX
PI   Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;

DR   WPI; 2003-449558/42.
DR   N-PSDB; AAL61293.
XX
PT   New immunogenic analogue of a polymeric protein, useful for preparing a
PT   composition for treating inflammatory diseases e.g. arthritis.
XX
PS   Claim 20; Page 109-110; 196pp; English.
XX
CC   The invention relates to immunogenic analogues of multimeric proteins
CC   such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC   factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC   analogues. The immunogenic analogue is useful for preparing a composition
CC   for treating inflammatory diseases, e.g., arthritis. It is also used in
CC   gene therapy. The present sequence is a fusion construct which comprises
CC   2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes
CC   P30 and P2. This sequence is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 285 AA;

Query Match   61.8%; Score 430; DB 6; Length 285;
Best Local Similarity   64.9%; Pred. No. 2.1e-42;
Matches   87; Conservative 17; Mismatches 30; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||| : |||
Db   1 MRMLLHLSLLALGAAYVAVAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
              |||:|||:||||:||||||| : ||||| |:||:|||||||| ||||||||| :|||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
              |||||:||||||||
Db   121 BFLGVMNTEWIIES 134

RESULT 14
ID   AAO30458
AC   AAO30458;
XX
DT   22-SEP-2003 (first entry)
XX
DE   hIL5-P2-P30-hIL5 (hIL5.35) fusion construct protein.
XX
KW   Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW   tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
KW   IL5; epitope; human; tetanus toxoid; chimeric.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
FH
FT   Key   Location/Qualifiers
FT   Peptide   1..19
FT   /note= "Human IL5 leader peptide"
FT   Protein   20. .285
FT   /note= "Mature hIL5.35 protein"
XX
PN   WO2003042244-A2.
XX
PD   22-MAY-2003.
XX
PF   15-NOV-2002; 2002WO-DK000764.
XX
PR   16-NOV-2001; 2001DK-00001702.
PR   16-NOV-2001; 2001US-0331575P.
XX
PA   (PHAR-) PHARMEXA AS.
PA   (KLYS/) KLYSNER S.
PA   (NIEL/) NIELSEN F S.

PA (BRATT/) BRATT T.
PA (VOLD/) VOLDBORG B.
PA (MOUR/) MOURITSEN S.
XX
PI Klysner S, Nielsen PS, Bratt T, Voldborg B, Mouritsen S;
XX
DR WPI; 2003-449558/42.
DR N-PSDB; AAL61294.
XX
PT New immunogenic analogue of a polymeric protein, useful for preparing a
PT composition for treating inflammatory diseases e.g. arthritis.
XX
PS Claim 20; Page 112-113; 196pp; English.
XX
CC The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC analogues. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is a fusion construct which comprises
CC 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes
CC P30 and P2. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 285 AA;
XX

```
Query Match             61.8%;  Score 430;  DB 6;  Length 285;
Best Local Similarity   64.9%;  Pred. No. 2.1e-42;
Matches   87;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy     1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
           |||:||||||||||||||||  || | |  |  ||:||||||| ||| | | | |:|||
Db     1 MRMLLHLSLLALGAAYVVYALPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy    61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
           ||| :||||| || | ||| :  | |::::||||| ||| |  | || | ||| |||||
Db    61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQPLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
           |||: ||:|||| ||
Db   121 EFLGVMNTEWIES 134
```

RESULT 15
AAB72616
ID AAB72616 standard; protein; 84 AA.
XX
AC AAB72616;
XX
DT 04-MAY-2001 (first entry)
XX
DE Canine interleukin-5 protein #2.
XX
KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction.
XX
OS Canis sp.
XX
PN WO200111049-A2.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021651.
XX
PR 10-AUG-1999; 99US-0371615.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Guo H, Lawton R, Mermer B, Aiyappa AP;
XX
DR WPI; 2001-191542/19.
DR N-PSDB; AAF74305.
XX

PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
PS Example 1; Fig 1; 48pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is one
CC version of the IL-5 protein shown in the specification
XX
SQ Sequence 84 AA;
XX

```
Query Match             61.6%;  Score 429;  DB 4;  Length 84;
Best Local Similarity   100.0%;  Pred. No. 4.5e-43;
Matches   84;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60

Qy    61 QLCIKEVFQGIDTLKNQTAHGEAV 84
           ||||||||||||||||||||||||
Db    61 QLCIKEVFQGIDTLKNQTAHGEAV 84
```

Search completed: August 4, 2005, 17:07:11
Job time : 137.538 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:　　　　　August　4, 2005, 16:59:07 ; Search time 26.3695 Seconds
　　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　　　488.938 Million cell updates/sec

Title:　　　　　US-10-787-382-5
Perfect score:　696
Sequence:　　　　1 MRMLLNLSILALGAAVVSAF.........FLDYLQVFLGVINTEWTPES 134

Scoring table:　BLOSUM62
　　　　　　　　　Gapop 10.0 , Gapext 0.5

Searched:　　　　283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:　283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 100 summaries

Database :　　　PIR_79:*
　　　　　　1: pir1:*
　　　　　　2: pir2:*
　　　　　　3: pir3:*
　　　　　　4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	551	79.2	134	2	JC5116	interleukin-5 prec
2	430	61.8	134	1	A28477	interleukin-5 prec
3	376	54.0	133	1	ICMS5	interleukin-5 prec
4	361	51.9	132	1	A48418	interleukin-5 prec
5	83.5	12.0	1199	2	G69698	RNA polymerase (be
6	78.5	11.3	258	2	T47758	hypothetical prote
7	77.5	11.1	331	2	G83876	hypothetical prote
8	77	11.1	478	2	T33735	hypothetical prote
9	74.5	10.7	1232	2	B39432	hypothetical prote
10	73.5	10.7	253	2	T47757	hypothetical prote
11	72.5	10.6	207	2	C71914	phosphoserine phos
12	72.5	10.4	451	2	S33816	hypothetical prote
13	72.5	10.4	649	2	S33813	kinesin light chai
14	72.5	10.4	677	2	S33814	kinesin light chai
15	72.5	10.4	686	2	S33815	kinesin light chai
16	72	10.3	253	2	C97331	arac-type DNA-bind
17	72	10.3	401	2	S28653	hypothetical prote
18	71	10.2	216	2	B6498	hypothetical prote
19	71	10.2	300	2	F84594	hypothetical prote
20	71	10.2	328	2	F64187	p-aminobenzoate sy
21	71	10.2	446	2	S76228	hypothetical prote
22	71	10.2	461	2	T38698	noc1 protein - fis
23	71	10.2	544	2	T42932	virion tegument pr
24	70.5	10.1	1055	2	T10432	DNA-directed RNA p
25	70	10.1	215	2	F45355	ORF2 protein - Aut
26	70	10.1	933	2	A59250	myosin - Acetabula
27	70	10.1	1871	2	D96698	probable DNA polym
28	70	10.1	1894	2	T02155	DNA-directed DNA p
29	69.5	10.0	1188	2	JC4889	phosphatidylinosit
30	69	9.9	215	2	B72854	AcOrf-34 protein -
31	69	9.9	346	2	S66958	UPB1 protein - yea
32	69	9.9	437	2	S50006	preprotein translo
33	69	9.8	759	2	F64662	trans-Golgi membra
34	68.5	9.8	189	2	D89966	AcMNPV orf34 - Bom
35	68.5	9.8	190	2	S23712	interferon alpha-I
36	68.5	9.8	638	2	A82115	hypothetical prote
37	68.5	9.8	709	2	T32089	hypothetical prote
38	68.5	9.8	756	2	T12697	probable membrane
39	68.5	9.8	1102	2	S65235	probable membrane
40	68	9.8	304	2	T41780	NADH2 dehydrogenas
41	68	9.8	414	2	B23431	truncated transpos
42	68	9.8	416	2	G84311	interferon alpha-I
43	68	9.8	529	2	T35282	hypothetical prote
44	68	9.8	767	1	S35306	probable two compo
45	67.5	9.7	1621	2	CO2PCD	phytoene dehydroge
46	67.5	9.7	247	2	A82255	cdc10 start contro
47	67.5	9.7	1189	2	C69272	hypothetical prote
48	67	9.6	189	1	JC6118	hypothetical prote
49	67	9.7	317	2	IVBOIC	SH2-containing ino
50	67	9.6	356	2	S15156	interferon alpha-I
51	67	9.6	437	2	S15156	hypothetical prote
52	67	9.6	463	2	G86761	drug-export protei
53	67	9.6	520	2	T37844	hypothetical prote
54	67	9.6	570	2	H71977	SCF complex protei
55	66.5	9.6	2311	2	D86793	skeletal myosin -
56	66.5	9.6	274	2	T06161	DNA-directed RNA p
57	66.5	9.6	1625	2	T21284	hypothetical prote
58	66	9.5	2325	2	T02235	probable sensor fo
59	66	9.5	248	2	A46652	probable sensor fo
60	66	9.5	368	2	A69774	acetyl-CoA carboxy
61	66	9.5	454	2	T01470	acetyl-CoA carboxy
62	66	9.5	248	2	A69774	glucosamine-6-phos
63	66	9.5	583	2	S40305	integrase homolog
64	65.5	9.4	756	2	S55805	diphosphate-fructo
65	65.5	9.4	590	2	H71977	multicystatin - po
66	65.5	9.4	119	1	T37844	alpha-toxin - Clos
67	65.5	9.4	1957	2	A59294	rhoptry protein -
68	65.5	9.4	360	2	G87441	glycine-tRNA ligas
69	65	9.4	295	2	A69636	hypothetical prote
70	65	9.3	377	2	AB1991	RNA-export mediato
71	65	9.3	538	2	S67766	chaperonin - Caeno
72	65	9.3	549	2	JC4083	hypothetical prote
73	65	9.3	549	2	T24508	MG068 homolog D02_
74	65	9.3	664	1	JX0336	succinate dehydrog
75	65	9.3	738	1	S51380	protein kinase STE
76	65	9.3	886	2	AD0831	probable acyl-CoA
77	65	9.3	1081	2	AD0831	pleiotropic drug r
78	65	9.3	1460	2	T00095	hypothetical prote
79	65	9.3	1685	2	S15040	acetyl-CoA carboxy
80	65	9.3	210	2	F64200	thymidylate kinase
81	65	9.3	220	2	A97953	multidrug efflux p
82	65	9.3	225	2	S73585	transcription regu
83	65	9.3	246	2	E95085	typeII secretion
84	65	9.3	328	2	B85940	type III secretion
85	64.5	9.3	328	2	F91094	type III secretion
86	64.5	9.3	451	1	JC6180	stearoyl-CoA 9-des
87	64.5	9.3	1	2	B90507	gamma-glutamyltran
88	64.5	9.3	478	2	B90507	two-component sens
89	64.5	9.3	479	2	AD1263	typeIII secretion
90	64.5	9.3	524	2	G90109	T-complex protein
91	64.5	9.3	536	2	B90507	conserved hypothet
92	64.5	9.3	702	2	D87631	NADH2 dehydrogenas
93	64.5	9.3	823	2	T12146	protein P1003.1 [i
94	64.5	9.3	1570	2	G86162	hypothetical prote
95	64.5	9.3	536	2	D87631	conserved hypothet
96	64.5	9.3	702	2	T12146	NADH2 dehydrogenas
97	64.5	9.3	823	2	G86162	protein P1003.1 [i
98	64	9.3	1570	2	AC2012	hypothetical prote
99	64	9.2	155	2	T12777	hypothetical prote
100	64	9.2	212	2	I67408	chorionic somatoma

ALIGNMENTS

RESULT 1
JC5116
interleukin-5 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
R;Mertens, B.; Gobright, E.; Seow, H.F.
A;Accession: JC5116
A;Molecule type: mRNA
A;Reference number: JC5116
A;Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.
Gene 176, 273-274, 1996
A;Cross-references: UNIPROT:P52173; EMBL:267872; NID:g1113120; PIDN:CAA91779.1; PID:g111
A;Residues: 1-134 <MER>
A;Experimental source: lymphocytes
C;Comment: This protein plays a role in the eosinophilia associated with parasitic disea
C;Genetics:
A;Gene: IL-5
A;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: interleukin-5 #status predicted <MAT>
F;63/Disulfide bonds: interchain (to 105) #status predicted
F;76,90/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;105/Disulfide bonds: interchain (to 63) #status predicted

Query Match   79.2%; Score 551; DB 2; Length 134;
Best Local Similarity 79.9%;   Pred. No. 4.9e-47;
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPENKNH 60
            |:|:|||||||||| |||:|||||||||||||||||||||||||||||||||||:||
Db   1 MRMLHLTLVALGAAYVCANAVSTMNRLVAETLTLLSSHRTLLIGDGNLMIPPQHTNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
            |||||||||||||||||||||:|||::||||||||||||||||| |||||||||||||
Db   61 QLCIEEVFQGIDTLKNQTAQGDAVKKIFQNLSLIKKYIDLQKRKCGGERWRVKQFLDYLQ 120

Qy   121 VFLGVINTEWTPBS 134
            ||||||||||||
Db   121 VFLGVINTEWTMES 134

RESULT 2
A28477
interleukin-5 precursor - human
N;Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d
C;Species: Homo sapiens (man)
A;Molecule type: DNA
A;Date: 01-Dec-1989 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A28477; A33883; A26112; A39881; JX0106; S15775
R;Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Mayo, G.; Clutterbuck, B.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6629-6633, 1987
A;Reference number: A28477; MUID:88059042; PMID:2824500
J. Biol. Chem. 262, 16580-16584, 1987
A;Title: Molecular cloning and structure of the human interleukin-5 gene.
A;Reference number: A28477; MUID:88059042; PMID:2824500
A;Accession: A28477
A;Molecule type: DNA
A;Residues: 1-134 <TAN>
A;Cross-references: GB:J02971; NID:g186340; PIDN:AAA98620.1; PID:g386823
A;Residues: 1-134 <CAM>
A;Accession: A33883
A;Molecular cloning, nucleotide sequence, and expression of the gene encoding hum
A;Reference number: A33883; MUID:88016145; PMID:3498940
R;Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.
J. Biol. Chem. 262, 16580-16584, 1987

Query Match   79.2%; Score 551; DB 2; Length 134;
Best Local Similarity 79.9%;   Pred. No. 4.9e-47;
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPENKNH 60
            |:|:|||||||||| |||:|||||||||||||||||||||||||||||||||||:||
Db   1 MRMLHLTLVALGAAYVCANAVSTMNRLVAETLTLLSSHRTLLIGDGNLMIPPQHTNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
            |||||||||||||||||||||:|||::||||||||||||||||| |||||||||||||
Db   61 QLCIEEVFQGIDTLKNQTAQGDAVKKIFQNLSLIKKYIDLQKRKCGGERWRVKQFLDYLQ 120

Qy   121 VFLGVINTEWTPBS 134
            ||||||||||||
Db   121 VFLGVINTEWTMES 134

A;Accession: A26112
A;Molecule type: mRNA
A;Residues: 1-134 <AZU>
A;Cross-references: GB:X04688; NID:g33835; PIDN:CAA28390.1; PID:g33836
R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmell
de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hume
A;Reference number: A39881; MUID:88041112; PMID:2823259
A;Accession: A39881
A;Status: not compared with conceptual translation
A;Accession: A39881
A;Molecule type: mRNA
R;Proudfoot, A.E.I.; Davies, J.G.; Turcatti, G.; Wingfield, P.T.
FEBS Lett. 283, 61-64, 1991
A;Title: Human interleukin-5 expressed in Escherichia coli: assignment of the disulfide b
A;Reference number: S15775; MUID:91243878; PMID:2037074
A;Contents: annotation; disulfide bonds
R;Minamitake, Y.; Kodama, S.; Katayama, T.; Adachi, H.; Tanaka, S.; Tsujimoto, M.
J. Biochem. 107, 292-297, 1990
A;Cross-references: GDB:120097; OMIM:147850
A;Contents: annotation; disulfide bonds; glycosylation sites
C;Genetics:
A;Gene: GDB:IL5
A;Cross-references: GDB:120097; OMIM:147850
A;Map position: 5q31.1-5q31.1
A;Introns: 48/3; 59/3; 102/3
A;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: interleukin-5 #status predicted <MAT>
F;22/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;47,90/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;63/Disulfide bonds: interchain (to 105) #status experimental
F;105/Disulfide bonds: interchain (to 63) #status experimental

Query Match   61.8%; Score 430; DB 1; Length 134;
Best Local Similarity 64.9%;   Pred. No. 4e-35;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPENKNH 60
            |||:|||||||||||||::| |||||||||||||||::||||||||||||||:|||
Db   1 MRMLHLSLLALGAAYVYALPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
            |||:||||||||| || |||| |||::||||||||||| || |||||||||:|||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFQNLSLIKKYIDQKXKCGGERWRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPBS 134
            |||||||||||| |
Db   121 EFLGVMNTEWIES 134

RESULT 3
ICMS5
interleukin-5 precursor - mouse
N;Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil di
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00807; A38758; A24898; JS0077; PH0102; B39881
R;Campbell, H.D.; Sanderson, C.J.; Wang, Y.; Hort, Y.; Martinson, M.E.; Tucker, W.Q.J.; f
Eur. J. Biochem. 174, 345-352, 1988
A;Title: Isolation, structure and expression of cDNA and genomic clones for murine eosino
n-5.
A;Reference number: S00807; MUID:88254802; PMID:3133208
A;Accession: S00807
A;Molecule type: DNA
A;Residues: 1-133 <CAM>
A;Cross-references: UNIPROT:P04401; EMBL:X06271; NID:g52685; PIDN:CAA29607.1; PID:g52686
A;Accession: A38758
A;Molecule type: mRNA
A;Residues: 1-133 <CAM2>

A;Cross-references: EMBL:X06270; NID:g52687; PIDN:CAA29606.1; PID:g52688
R;Kinashi, T.; Harada, N.; Severinson, E.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma,
Nature 324, 70-73, 1986
A;Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with
A;Note;
A;Experimental source:
A;Reference number: A24898; MUID:87065032; PMID:3024009
A;Superfamily: interleukin-5
A;Accession: A24898
A;Molecule type: mRNA
A;Residues: 1-133 <KIN>
A;Cross-references: EMBL:X04601; NID:g54898; PIDN:CAA28266.1; PID:g54899
R;Mizuta, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.
Growth Factors 1, 51-57, 1988
A;Title: Molecular cloning and structure of the mouse interleukin-5 gene.
A;Reference number: JS0077; MUID:90180853; PMID:3078564
A;Residues: 1-133 <MIZ>
A;Molecule type: DNA
A;Accession: JS0077
R;Takahashi, T.; Yamaguchi, N.; Mita, S.; Yamaguchi, Y.; Suda, T.; Tominaga, A.; Kikuchi
Mol. Immunol. 27, 911-920, 1990
A;Title: Structural comparison of murine T-cell (B151K12)-derived T-cell-replacing facto
A;Reference number: PH0102; MUID:91015093; PMID:2215480
A;Accession: PH0102
A;Molecule type: protein
A;Residues: 21-45,'X',47 <TAK>
R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum
de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.
A;Reference number: A39881; MUID:88041112; PMID:2823259
A;Accession: B39881
A;Status: preliminary; not compared with conceptual translation

Query Match   54.0%;   Score 376;   DB 1;   Length 133;
Best Local Similarity   56.8%;   Pred. No. 8.2e-30;
Matches 75;   Conservative 21;   Mismatches 34;   Indels 2;   Gaps 1;

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Qy    2 RMLLNLSLIALGAAYVSAFAVENPMNRLVAETLTLLLSTHRTWLIGDGNLMIPTPENKNHQ 61
        ||||:|||:||||||||||:|||||||:||||||:||| : :|||||||||||||||||
Db    3 RMLHLSVITLSCVW--AYAMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVFTHKNHQ 60

Qy   62 LCIKEVFQGIGTDLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQV 121
        ||||||||||||||:||||   |||||||||||||:|||||| ||||||||| |:|||
Db   61 LCIGEIFQGLDILKNQTVRGGTVEMLFQNLSLIKKYIDRQKEKCGEERRTRHFLDYIQ 120

Qy  122 FLGVINTEWTPE 133
        ||||:||:||||
Db  121 FLGVMSTEWAME 132
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RESULT 4
A48418
Interleukin-5 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A48418; S37641
R;Uberla, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstei
Cytokine 3, 72-81, 1991
A;Title: The rat interleukin-5 gene: characterization and expression by retroviral gene
A;Reference number: A48418; MUID:91355638; PMID:1653053
A;Accession: A48418
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-132 <UBE>
A;Cross-references: UNIPROT:Q08125; EMBL:X54419; NID:g313254; PIDN:CAA38283.1; PID:g3132
A;Experimental source: cell line TR5-1
A;Note; sequence extracted from NCBI backbone (NCBIN:63651, NCBIP:63652)
A;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-132/Product: interleukin-5 #status predicted <MAT>
F;45,74,88/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;61/Disulfide bonds: interchain (to 103) #status predicted
F;103/Disulfide bonds: interchain (to 61) #status predicted

Query Match   51.9%;   Score 361;   DB 1;   Length 132;
Best Local Similarity   54.9%;   Pred. No. 2.4e-28;
Matches 73;   Conservative 21;   Mismatches 37;   Indels 2;   Gaps 1;

```
Qy    1 MRMLLNLSLIALGAAYVSAFAVENPMNRLVAETLTLLLSTHRTWLIGDGNLMIPTPENKNH 60
        ||||||||||:|||||||||||||||||||||||:||| : :|||||||||||||| ||||
Db    1 MRMLCLNVLTLSCVW--AYAMEIPMSTVVKETLTQLSTHRALLTSNETMRLPVFTHKNHQ 58

Qy   61 QLCIKEVFQGIGTDLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQ 120
        |||||||||||||:||||   |||||||||||||:|||||| ||||||||| |:||||
Db   59 QLCIGEIFQGLDILKNQTVRGGTVEILFQNLSLIKKYIDGQKEKCGEERRTRHFLDYIQ 118

Qy  121 VFLGVINTEWTPE 133
         ||||:||:||||
Db  119 EFLGVMSTEWAME 131
```

RESULT 5
G69698
RNA polymerase (beta' subunit) rpoC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: G69698
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galero
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Koetter, P.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel,
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: G69698
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1199 <KUN>
A;Cross-references: UNIPROT:P37871; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11884.
C;Genetics:
A;Experimental source: strain 168
A;Gene: rpoC
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match   12.0%;   Score 83.5;   DB 2;   Length 1199;
Best Local Similarity   27.1%;   Pred. No. 7.1;
Matches 35;   Conservative 20;   Mismatches 41;   Indels 33;   Gaps 6;

```
Qy    1 MRMLLNLSLIAL-GAAYVSAFAVENPMNRLVAETLTLLLSTHRTWLIGDGNLMIPTPENKN 59
         :|:|:|| :|| :| ||| :|| |||:|:::|:: : :|| : : |
Db  114 MGLVLDMSPRALEEVIFASTVVTDPAN----------------------TPLEKK 147

Qy   60 HQLCIKEVFQGIGTDLKN-QTAHG-EAVDKLFQNLSLIKE--HIERQKKRCAGE-RWRVT 113
         | ||||||| ::  :| |   |  |:|       :   |:|:|  |  :|:|:
Db  148 QLLSEKBYRAYLDKYGNKFQASMGAEAAIHKLLQDIDLVKEVDMLKEELKTSGGQRRTRAI 207
```

RESULT 6
T47758
hypothetical protein F2413.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47758
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: 224475
A;Experimental source: UNIPROT:Q9MIK0; EMBL:AL138655
A;Cross-references: UNIPROT:Q9MIK0; EMBL:AL138655
A;Residues: 1-258 <NYA>
A;Molecule type: DNA
A;Status: preliminary
A;Accession: T47758
A;Map position: 3
A;Note: 109/3
A;Introns: 109/3
C;Genetics:
C;Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match   11.3%;   Score 78.5;   DB 2;   Length 258;
Best Local Similarity   26.8%;   Pred. No. 3.5;
Matches   22; Conservative   15; Mismatches   38;   Indels   7;   Gaps   2;

Qy   28 RLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKSVPQGID---TLKNQTAHGEA 83
           :||:|::||:| :|:|::||||||||||||||||||| ||:|| ::|||:||:
Db 161 KAVANYISTVSATR---LGDNEWVQISSSKIHNFSISNVLSGLEEDRPVLVDMSSSRSQ 217

Qy   84 VDKLFQNLSLIKEHIERQKKRC 105
           |||||||||||:|||||:||:
Db 218 GERLFYTLHLQVEKIENYXLNC 239

RESULT 7
G83876
hypothetical protein BH1815 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
A;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83876
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <STO>
A;Cross-references: UNIPROT:Q9KBV9; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB055
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1815

Query Match   11.1%;   Score 77.5;   DB 2;   Length 331;
Best Local Similarity   26.7%;   Pred. No. 5.9;
Matches   27; Conservative   20; Mismatches   43;   Indels   11;   Gaps   4;

Qy   7 LSLLA---LGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLC 63
          |||:| || ::|| |::| : || |:|| :|:|::|||||||||||||||||||||
Db   86 LRLLADALTTASFISKEEFTEQMINKLKKLTSHRLADHL----DNRLLVP-PDRGNRE-- 137

Qy   64 IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKR 104
          |:|:|:|:|:||||:|||| |||:|||||||||||||:||:
Db 138 VQELIKTVHLLHDVIKHGEVIRYQYGQYNLTKEFTLRENGR 178

RESULT 8
T33735

hypothetical protein H34C03.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A;Description: The sequence of C. elegans cosmid H34C03.
A;Reference number: Z21394
A;Accession: T33735
R;Kalicki, J.; Gibson, A.
submitted to the EMBL Data Library, October 1998
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-478 <KAL>
A;Cross-references: UNIPROT:Q9TYY7; EMBL:AF100662; PIDN:AAC68976.1; GSPDB:GN000022; CBSP:H
A;Experimental source: strain Bristol N2; clone H34C03
A;Accession: T33735
C;Genetics:
A;Gene: CBSP:H34C03.1
A;Map position: 4
A;Introns: 57/1; 103/2; 185/3; 283/2; 347/3; 426/3
C;Superfamily: Caenorhabditis elegans hypothetical protein H34C03.1

Query Match   11.1%;   Score 77;   DB 2;   Length 478;
Best Local Similarity   27.3%;   Pred. No. 10;
Matches   33; Conservative   20; Mismatches   46;   Indels   22;   Gaps   5;

Qy   6 NLSLLALGAAYVSAFAVENPMNRLVAETLTL----LSTHRTWLIGDGNLMIPTP----- 55
          |||||:|| ::|| ||:| : ||| |:|:| |:|:|::|||||||||||||
Db 261 NKSLLELGWKQQTALEAILEEAILERLESESVTQSEVESSALHKTFLVVKABAPAPQPVKKIDV 320

Qy   56 -----ENKNHQLCIKSVPQG---IDTLKNQTAHGEAVDKLFQNLSLIKEHI--ERQKKR 104
             ::|||:|::|:|| ::::|:||:|||:|||| |||:|||||||:|: ||:||:
Db 321 EVRNQDQKPEVIVIEKQTGSERTDIDMVFSGTPLSBA-DXLSASKSAVARDVLLDGSBGR 379

Qy 105 C 105
          |
Db 380 C 380

RESULT 9
B39432
ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis
N;Alternate names: ATP-dependent exonuclease synthesis protein AddA
C;Species: Bacillus subtilis
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
C;Accession: B39432; H69582
R;Kooistra, J.; Venema, G.
J. Bacteriol. 173, 3644-3655, 1991
A;Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-c
A;Reference number: A39432; MUID:91267926; PMID:1646786
A;Accession: B39432
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1232 <KOO>
A;Cross-references: UNIPROT:P23478; GB:M63489; NID:g142438; PIDN:AAA22201.1; PID:g142440
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauei
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A65580; MUID:98044033; PMID:9384377
A;Accession: H69582
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1232 <KUN>

Qy 114 KFLDYLQVF 122
          |:|:|:|:|
Db 208 KRLEVLEAP 216

A;Cross-references: GB:Z99105; GB:AL009126; NID:g2633260; PIDN:CAB12903.1; PID:e1183065;
A;Experimental source: strain 168
C;Genetics:
C;Keywords: nucleotide binding; P-loop
A;Gene: adda
F;30-37/Region: nucleotide-binding motif A (P-loop)

Query Match   10.7%; Score 74.5; DB 2; Length 1232;
Best Local Similarity   22.2%; Pred. No. 56;
Matches   24; Conservative   24; Mismatches   37; Indels   23; Gaps   4;

```
Qy     22 VENPMNRLVAETLTLLSTHRTWLIG--DGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79
             ||| |  ||    :::|||||||  |||||||||||||||||||||||||||||
Db    633 IDNPY-----QDIPLASVLRSPIVGADENELSLIRLENKTAPY-----YEAMKDYLA 679

Qy     80 HGEAVDKLFQNLSLIKEHIERQK--------KRCAGERWRVTKFLDYL 119
             ||||||||||||||||||||        |||||||:||||:
Db    680 AGDRSDELYQKLNTFYGHLQKWRAFSKNHSVSELIWEVYRDTKYMDYV 727
```

RESULT 10
T47757
hypothetical protein F24I3.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47757
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
R;Reference number: Z24475
A;Accession: T47757
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <NYA>
A;Cross-references: UNIPROT:Q9M1KJ; EMBL:AL138655
A;Experimental source: cultivar Columbia; BAC clone F24I3
C;Genetics:
A;Map position: 3
A;Introns: 104/3
A;Note: F24I3.50
C;Superfamily: Arabidopsis thaliana hypothetical protein F24I3.60

Query Match   10.6%; Score 73.5; DB 2; Length 253;
Best Local Similarity   27.1%; Pred. No. 11;
Matches   23; Conservative   15; Mismatches   34; Indels   13; Gaps   3;

```
Qy     28 RLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGID-------TLKNQTAH 80
          |||  :  | :| :::  ||||||||||||||||||||||||||       ::||:
Db    156 KAVASYLSTVSATR---LGNEVMVQVSSSKIHNFSISNVLGGIEEDGFVLVDVSSSRSQ 212

Qy     81 GEAVDKLFQNLSLIKEHIERQKKRC 105
          |||||||||||||||||||||||
Db    213 GE---RLFYTLHLQVENMDDYKINC 234
```

RESULT 11
C71914
phosphoserine phosphatase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: C71914
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: C71914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <ARN>
A;Cross-references: UNIPROT:Q9ZLI2; GB:AE001491; GB:AE001439; NID:g4155127; PIDN:AAD0617
C;Genetics:

A;Gene: serB
C;Superfamily: phosphoserine phosphatase

Query Match   10.4%; Score 72.5; DB 2; Length 207;
Best Local Similarity   29.8%; Pred. No. 10;
Matches   31; Conservative   14; Mismatches   34; Indels   25; Gaps   5;

```
Qy      9 LLALGAAYVSAFAVE-NPMDRLVA--------------------EFTLTLLSTHRTWLIGDGNLM 51
            |  |     | :|  ||| ||                    ::::||:|||||||:||||||
Db    109 LLNLDAAFSNTLIVENNALNGLVTGHNMFSYSKGEMLLALQRLLNISKDRTLVVGDGAND 168

Qy     52 IPTPENKNHQLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIK 95
          ||||||||||||||||||||||||||||:  ||  ::|| ||
Db    169 LSMFKHAH-----IKIAFNAKEILKQHATH--CIDK--PNLALIK 204
```

RESULT 12
S33816
kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S33816
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33816; MUID:93267648; PMID:8496962
A;Accession: S33816
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-451 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L08258; NID:g161531; PID:g161532

Query Match   10.4%; Score 72.5; DB 2; Length 451;
Best Local Similarity   25.9%; Pred. No. 27;
Matches   21; Conservative   19; Mismatches   30; Indels   11; Gaps   3;

```
Qy     46 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKK 103
          ||||                ::||: :|||||::|| || ||:||:|||||||||||||
Db     15 GQGNL------SQEQIITGTREVIKGLBQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy    104 RCAGERWRVTKFLDYLQVFLG 124
          :  ||||||||||: ::|||
Db     66 LVBEKYDIIEKSLESLELGLG 86
```

RESULT 13
S33813
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33813
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:93267648; PMID:8496962
A;Accession: S33813
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-649 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L10233; NID:g161525; PID:g161526

Query Match   10.4%; Score 72.5; DB 2; Length 649;
Best Local Similarity   25.9%; Pred. No. 41;
Matches   21; Conservative   19; Mismatches   30; Indels   11; Gaps   3;

```
Qy     46 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKK 103
          ||||                ::||: :|||||::|| || ||:||:|||||||||||||
Db     15 GQGNL------SQEQIITGTREVIKGLBQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy    104 RCAGERWRVTKFLDYLQVFLG 124
          :  ||||||||||: ::|||
Db     66 LVBEKYDIIEKSLESLELGLG 86
```

RESULT 14
S33814
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33814
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:93267648; PMID:8496962
A;Accession: S33814
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-677 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L10234; NID:g161527; PID:g161528

Query Match   10.4%;   Score 72.5;   DB 2;   Length 677;
Best Local Similarity   25.9%;   Pred. No. 43;
Matches   21;   Conservative   19;   Mismatches   30;   Indels   11;   Gaps   3;

Qy   46 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKK 103
          |:|| || |:|: ||:: |:: | :|: ::|:
Db   15 GQGNL------SQEQIITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy   104 RCAGERWRVTKFLDYLQVFLG 124
         : ||:|:||:|| ||
Db   66 LVEEKTDIIEKSLESLELGLG 86

RESULT 15
S33815
kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S33815; S36727
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:93267648; PMID:8496962
A;Accession: S33815
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-686 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L10235
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
submitted to the EMBL Data Library, February 1993
A;Reference number: S36727
A;Accession: S36727
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-568,'A',570-686 <WE2>
A;Cross-references: EMBL:L10235; NID:g161529; PID:g161530

Query Match   10.4%;   Score 72.5;   DB 2;   Length 686;
Best Local Similarity   25.9%;   Pred. No. 44;
Matches   21;   Conservative   19;   Mismatches   30;   Indels   11;   Gaps   3;

Qy   46 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKK 103
          |:|| || |:|: ||:: |:: | :|: ::|:
Db   15 GQGNL------SQEQIITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy   104 RCAGERWRVTKFLDYLQVFLG 124
         : ||:|:||:|| ||
Db   66 LVEEKTDIIEKSLESLELGLG 86

Search completed: August 4, 2005, 17:11:59
Job time : 30.3695 secs

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                         GenCore version 5.1.6
                         Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:              August   4, 2005, 16:50:50 ; Search time 121.622 Seconds
                                                  (without alignments)
                                                  564.193 Million cell updates/sec

Title:               US-10-787-382-5
Perfect score:       696
Sequence:            1 MRMLLNLSLLALGAAYVSAP.........FLDYLQVPLGVINTEWTPES 134

Scoring table:       BLOSUM62
Search:              Gapop 10.0 , Gapext 0.5

Searched:            1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:     1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

Database :     UniProt_03:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	696	100.0	134	1	IL5_CANPA	Q95J76 canis famil
2	591	84.9	134	1	IL5_FELCA	O77515 felis silve
3	586	84.2	134	1	Q9TSD7	Q9tsd7 felis silve
4	578	83.0	134	2	Q9MYM5	Q9mym5 sus scrofa
5	571	82.0	118	2	Q9TVI0	O02699 canis famil
6	567	81.5	134	1	IL5_HORSE	O02699 equus cabal
7	551	79.2	134	1	IL5_BOVIN	P52173 bos taurus
8	536	77.0	132	1	IL5_SHEEP	O28586 ovis aries
9	448	64.4	134	2	Q8MKH1	Q8mkh1 saimiri sci
10	430	61.8	134	1	IL5_HUMAN	P05113 homo sapien
11	429	61.6	134	1	IL5_CERTO	P05113 homo sapien
12	426	61.2	134	1	IL5_MACMU	P48093 macaca mula
13	414.5	59.6	135	1	IL5_CAVPO	O08987 cavia porce
14	388	55.7	132	1	IL5_MERUN	Q9es19 meriones un
15	388	55.7	132	1	IL5_SIGHI	062575 sigmodon hi
16	376	54.0	133	1	IL5_MOUSE	P04401 mus musculu
17	372	53.4	139	1	IL5_MACEU	Q9xt91 macropus eu
18	361	51.9	132	1	IL5_RAT	008125 rattus norv
19	354	50.9	132	2	Q9R2C9	Q9r2c9 rattus norv
20	214	30.7	48	2	Q6PVS2	Q6pvs2 ovis aries
21	109.5	15.7	40	2	Q9XT92	Q9xt92 sminthopsis
22	98.5	14.2	590	1	MP44_MYXVL	Q9q8q1 myxoma viru
23	84	12.1	360	2	062M23	062m23 burkholderi
24	84	12.1	360	2	Q63S03	Q63s03 burkholderi
25	83.5	12.0	1199	2	RPOC_BACSU	Rpoc bacsu bacillus su
26	83	11.9	487	2	Q7R8B3	Q7r8b3 plasmodium
27	81.5	11.7	488	2	Q7ZUA6	Q7zua6 gallus gall
28	80.5	11.6	452	2	Q7ZZ1	075a46 ashbya goss
29	80.5	11.6	485	2	Q7ZZ1	Q7zzz1 gallus gall
30	79.5	11.4	610	2	Q9NA53	Q9na53 caenorhabdi
31	79	11.4	676	2	Q7YKV5	Q7ykv5 mapania par
32	78.5	11.3	258	2	Q9M1K0	Q9m1k0 arabidopsis
33	78.5	11.3	463	2	Q91WC6	Q91wc6 mus musculu
34	78.5	11.3	490	2	Q9JIT0	Q9jit0 mus musculu
35	77.5	11.1	331	2	Q9KBV9	Q9kbv9 bacillus ha
36	77.5	11.1	721	2	Q73PE9	Q73pe9 treponema d
37	77.5	11.1	1199	2	Q65PB4	Q65pb4 bacillus li
38	77	11.1	478	1	SECY_STRGB	Q59912 streptomyce
39	77	11.1	490	2	Q9TYY7	Q9tyy7 caenorhabdi
40	76.5	11.0	158	2	O96575	O96575 leucophaea
41	76.5	11.1	284	2	Q6FW99	Q6fw99 candida gla
42	75.5	11.1	490	2	Q8NDP7	Q8ndp7 homo sapien
43	75.5	10.8	490	2	Q8WVP7	Q8wvp7 homo sapien
44	75.5	10.8	655	2	Q96QZ5	Q96qz5 homo sapien
45	75	10.8	292	2	Q7MV24	Q7mv24 porphyromon
46	75	10.8	292	2	Q8PUD3	Q8pud3 methanosarc
47	74.5	10.7	1313	2	Q8PNY3	Q8pny3 xanthomonas
48	74.5	10.7	1232	1	ADDA_BACSU	P23478 bacillus su
49	74	10.7	241	2	Q8SKY6	Q8sky6 myosotis di
50	74	10.6	241	2	Q8SKZ3	Q8skz3 myosotis ra
51	74	10.6	302	2	Q831U2	Q831u2 enterococcu
52	74	10.6	355	2	Q72418	Q72418 listeria mo
53	73.5	10.6	395	2	Q9VK11	Q9vk11 drosophila
54	73.5	10.6	161	2	Q9M1K1	Q9m1k1 arabidopsis
55	73.5	10.6	253	2	Q6I105	Q6i105 drosophila
56	73	10.6	1293	2	Q6BNW7	Q6bnw7 debaryomyce
57	73.5	10.6	1835	2	Q8SKY3	Q8sky3 myosotis ma
58	73	10.6	241	2	Q8RVR0	Q8rvr0 helianthus
59	73	10.5	248	2	Q8PCA2	Q8pca2 xanthomonas
60	73	10.5	313	2	Q7XRA1	Q7xra1 oryza sativ
61	73	10.5	623	2	Q921P5	Q921p5 mus musculu
62	73	10.5	623	2	Q8K2B3	Q8k2b3 mus musculu
63	73	10.5	510	2	Q8W3A1	Q8w3a1 oryza sativ
64	73	10.5	418	2	Q9Z1I2	Q9z1i2 helicobacte
65	72.5	10.4	207	2	Q9CLF5	Q9clf5 pasteurella
66	72.5	10.4	229	2	Q8ZZS2	Q8zzs2 pyrobaculum
67	72.5	10.4	310	2	Q064B6	Q064b6 xanthomonas
68	72.5	10.4	313	2	Q8S1N1	Q8s1n1 oryza sativ
69	72.5	10.4	418	2	Q8GWT4	Q8gwt4 arabidopsis
70	72.5	10.4	510	2	Q6M0A6	Q6m0a6 methanococc
71	72.5	10.4	623	2	Q8IHQ8	Q8ihq8 plasmodium
72	72.5	10.4	664	2	Q6D8B3	Q6d8b3 erwinia car
73	73	10.5	827	1	DHSA_MOUSE	O5090 strongyloce
74	72.5	10.4	207	1	Q97DG5	Q97dg5 clostridium
75	72.5	10.4	253	2	Q8TQV4	Q8tqv4 methanosarc
76	72	10.3	296	1	YI_8_METSM	P22344 methanobrev
77	72	10.3	401	2	Q7TH69	Q7th69 lycoris pot
78	72	10.3	562	2	Q6YK77	Q6yk77 toxoplasma
79	72	10.3	692	2	Q7UEK7	Q7uek7 rhodopirell
80	72	10.3	239	1	Q7SCM8	Q7scm8 neurospora
81	71.5	10.3	534	2	Q6CS00	Q6cs00 kluyveromyc
82	71.5	10.3	595	2	Q98I62	Q98i62 little cher
83	71.5	10.3	664	2	Q9XZ06	Q9xz06 drosophila
84	71.5	10.3	823	2	Q92KQ9	Q92kq9 rhizobium m
85	71.5	10.3	907	2	O28292	O28292 archaeoglob
86	71.5	10.3	216	1	O00944	O00944 thelleria m
87	71	10.2	279	2	Q9SKT0	Q9skt0 arabidopsis
88	71	10.2	300	1	YB70_HAEIN	Y870_HAEIN haemophilus
89	71	10.2	328	1	P74390	P74390 synechocyst
90	71	10.2	446	1	P79065	P79065 schizosacch
91	71	10.2	461	1	TIP1_SCHPO	Q9ytp7 ateline her
92	71	10.2	544	2	Q8MYT8	Q8myt8 drosophila
93	71	10.2	827	2	Q9W3C9	Q9w3c9 drosophila
94	71	10.2	827	2	Q947M6	Q947m6 setaria ita
95	71	10.2	2321	2	Q7PYK6	Q7pyk6 anopheles g
96	70.5	10.1	320	2	Q8TSW7	Q8tsw7 methanosarc
97	70.5	10.1	347	2	Q6N9Z5	Q6n9z5 rhodopseudo
98	70.5	10.1	320	2	Q7SFG6	Q7sfg6 neurospora
99	70.5	10.1	455	2	Q6IWP4	Q6iwp4 brachydanio
100	70.5	10.1	480	2	Q6IWP4	Q6iwp4 brachydanio

ALIGNMENTS

```
RESULT 1
ID   IL5_CANFA      STANDARD;      PRT;   134 AA.
AC   Q95J76;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21334408; PubMed=11440633; DOI=10.1089/107999001750277835;
RA   Yang S., Sellins K.S., Weber B., McCall C.;
RT   "Canine interleukin-5: molecular characterization of the gene and
RT   expression of biologically active recombinant protein.";
RL   J. Interferon Cytokine Res. 21:361-367(2001).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   -------------------------------------------------------------------------
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CC   -------------------------------------------------------------------------
DR   EMBL; AF331920; AAL10716.1; -.
DR   EMBL; AF331919; AAL10715.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD067721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     21       By similarity.
FT   CHAIN        22    134       Interleukin-5.
FT   DISULFID     63    105       Interchain (with C-105) (By similarity).
FT   DISULFID    105     63       Interchain (with C-63) (By similarity).
FT   CARBOHYD     76     76       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15307 MW;  003C86D94D6FP4C6 CRC64;

Query Match             100.0%;  Score 696;  DB 1;  Length 134;
Best Local Similarity   100.0%;
Matches  134;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MRMLLNLSLLALGAAYVSAPAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRMLLNLSLLALGAAYVSAPAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60

Qy         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120

Qy        121 VFLGVINTEWTPES 134
              ||||||||||||||
Db        121 VFLGVINTEWTPES 134
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RESULT 2
IL5_FELCA
ID   IL5_FELCA      STANDARD;      PRT;   134 AA.
AC   O77515; O62740;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98452719; PubMed=9781459;
RA   Padrid P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT   "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL   Am. J. Vet. Res. 59:1263-1269(1998).
RN   [2]
RP   SEQUENCE OF 12-128 FROM N.A.
RA   Harley R., Day M.J., Gruffydd-Jones T.J., Harbour D.A., Helps C.R.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   -------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------------
DR   EMBL; AF025436; AAC64505.1; -.
DR   EMBL; AF051372; AAC05752.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD067721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     19       By similarity.
FT   CHAIN        20    134       Interleukin-5.
FT   DISULFID     63    105       Interchain (with C-105) (By similarity).
FT   DISULFID    105     63       Interchain (with C-63) (By similarity).
FT   CARBOHYD     76     76       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
FT   CONFLICT    104    105       KC -> NF (in Ref. 2).
FT   CONFLICT    108    111       ERWR -> KRWK (in Ref. 2).
FT   CONFLICT    114    114       K -> N (in Ref. 2).
FT   CONFLICT    117    117       D -> N (in Ref. 2).
FT   CONFLICT    121    121       V -> F (in Ref. 2).
FT   CONFLICT    125    126       VI -> LL (in Ref. 2).
SQ   SEQUENCE   134 AA;  15224 MW;  87D18DB8F8CAC820 CRC64;

Query Match             84.9%;  Score 591;  DB 1;  Length 134;
Best Local Similarity   85.1%;
Matches  114;  Conservative  11;  Mismatches   9;  Indels   0;  Gaps   0;

Qy          1 MRMLLNLSLLALGAAYVSAPAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
              ||||| ||||||||||||  | :|||||||||: ||||||||| |||||||||||| :||
Db          1 MRMLHLSLLALGAAYVSAIAVQSPMNRLVAETLALLSTHRTLLIGDGNLMIPTPEHNNH 60

Qy         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
              |||| |||||||||| |:   |:||:|||:|||||||||: |||::| |||| ||||||||
Db         61 QLCIEEVFQGIDTLKNRTVPGDAVEKLFRNLSLIKEHIDRQKKKCGGERRVKKFLDYLQ 120

Qy        121 VFLGVINTEWTPES 134
              ||||||||||||||
Db        121 VFLGVINTEWTPES 134
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Db          121 VFLGVINTEWTMES 134
                |||||||||||||| ||
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RESULT 3
Q9TSD7

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ID   Q9TSD7;     PRELIMINARY;    PRT;    134 AA.
AC   Q9TSD7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin 5.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vandegrifft E., Hughes K.J., O'Reilly K.L.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF068770; AAC27616.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR000186; Interleukin_5.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
SQ   SEQUENCE   134 AA;  15176 MW;  9A118B78F8CAC820 CRC64;

Query Match             84.2%;  Score 586;  DB 2;  Length 134;
Best Local Similarity   85.0%;  Pred. No. 2.1e-49;
Matches 113;  Conservative 11;  Mismatches 9;  Indels 0;  Gaps 0;

Qy    1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          |||||||||||||||||| ||||||||||||||||||||||||||||||:|| ||
Db    1 MRMLLHLSLLALGAAYVSAIAVQSPNRLVAETLALLSTHRTLLIGDGNLMIPTPEHNNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
          ||:|||||||||||||:|||::|:|::| ||:|||||||||||||||||||||||:|
Db   61 QLCIEEVFQGIDTLKNRTVPGDAVEKLFRNLSLIKEHIDRQKKKCGGERWRVKFLDYLQ 120

Qy  121 VFLGVINTEWTMES 133
          |||||||||| |
Db  121 VFLGVINTEWTIE 133
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RESULT 5
Q9TV10

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RA   Heegaard P.M.H.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ010088; CAB70611.2; -.
DR   EMBL; AJ133452; CAB38328.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
SQ   SEQUENCE   134 AA;  15191 MW;  B485D562A028A899 CRC64;

Query Match             83.0%;  Score 578;  DB 2;  Length 134;
Best Local Similarity   85.1%;  Pred. No. 1.3e-48;
Matches 114;  Conservative 8;  Mismatches 12;  Indels 0;  Gaps 0;

Qy    1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNH 60
          |||||||:||:||||||||||||||||||||||||||||||||||||||| :||
Db    1 MRMLLHLSLLGLGAAYVSAIAVENTMNRLVAETLTLLSIHRTLLIGDGNLMISTPVHTNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
          ||:|||||||||||||:||:  :|::|::||:|||||||:|||||:|| ||||||:||||
Db   61 QLCIEEVFQGIDTLKNQTARGDAVEKLFQNLSLIKEYIDRQKKNCGGERWRVTQFLDYLQ 120

Qy  121 VFLGVINTEWTMES 134
          |||||||||||| |
Db  121 VFLGVINTEWTMES 134
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ID   Q9TV10;     PRELIMINARY;    PRT;    118 AA.
AC   Q9TV10;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin-5 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091133; AAD46991.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13507 MW;  36A55663DD67C968C CRC64;
```

RESULT 4
Q9MYM5

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ID   Q9MYM5;     PRELIMINARY;    PRT;    134 AA.
AC   Q9MYM5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin-5.
GN   Name=Il-5;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20130134; PubMed=10663563;
RA   Sylvin H., Matvienko O., leonchiks A., Alving K., van der Ploeg I.;
RT   "Molecular cloning, expression, and purification of pig interleukin-
RT   5.";
RL   Immunogenetics 51:59-64(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,
```

```
Query Match             82.0%;  Score 571;  DB 2;  Length 118;
Best Local Similarity   93.8%;  Pred. No. 5.3e-48;
Matches 106;  Conservative 6;  Mismatches 1;  Indels 0;  Gaps 0;

Qy   18 SAFAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQ 77
          ||||||:|||||||||:|||||||||||||||||||||||||||||||||||||||||
Db    6 SAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQ 65

Qy   78 TAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEW 130
          ||||||||||||||||||||||||||||:|||:||:||:|:||||:||||||
Db   66 TAHGEAVDKLFQNLSLIKEHIERQKKRCAGKKWMKVTNFLNYLQLFLGVMNTEW 118
```

```
RESULT 6
ID   IL5_HORSE      STANDARD;      PRT;   134 AA.
AC   O02699;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vandergrifft B.V., Horohov D.W.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U91947; AAB51382.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    134       Interleukin-5.
FT   DISULFID     63    105       Interchain (with C-105) (By similarity).
FT   DISULFID    105     63       Interchain (with C-63) (By similarity).
FT   CARBOHYD     76     76       N-linked (GlcNAc...) (By similarity).
FT   CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15081 MW;  291484UB3E7A006D CRC64;

Query Match             81.5%;  Score 567;  DB 1;  Length 134;
Best Local Similarity   83.5%;
Matches  111;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDNLMIPTPENKNH 60
              ||||:||  |:||||||||:| |||:|||||||||||| ||| |||:|||||||||:||:|
Db          1 MRMLHLHLSVIALGAAYVCALAVESSPMNRLVAETLTLLSHRTLLIGDGNLMIPTPEHKNH 60

Qy         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
              |||:|||||||||||||:| | ||:||||||||||| :::|||:|:|||||||:::|||||
Db         61 QLCIEEVFQGIDTLKNQTVQGDAVAKLFQNLSLIKGYIDLQKKKCGGERWRVKQFLDYLQ 120

Qy        121 VFLGVINTEWTPB 133
              ||||||||||||  |
Db        121 EFLGVINTEWTIB 133
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RESULT 7
ID   IL5_BOVIN      STANDARD;      PRT;   134 AA.
AC   P52173;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=97075944; PubMed=8918267; DOI=10.1016/0378-1119(96)00252-1;
RA   Mertens B., Gobright E., Seow H.F.;
RT   "The nucleotide sequence of the bovine interleukin-5-encoding cDNA.";
RL   Gene 176:273-274(1996).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z67872; CAA91779.1; -.
DR   PIR; JC5116; JC5116.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     21
FT   CHAIN        22    134       Interleukin-5.
FT   DISULFID     63    105       Interchain (with C-105) (By similarity).
FT   DISULFID    105     63       Interchain (with C-63) (By similarity).
FT   CARBOHYD     76     76       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15229 MW;  0B3A2328BE7431F4 CRC64;

Query Match             79.2%;  Score 551;  DB 1;  Length 134;
Best Local Similarity   79.9%;
Matches  107;  Conservative   15;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDNLMIPTPENKNH 60
              ||||:|  |:||||||||:|.|.|:|:|||||||||||.|||.|||:|||||||| : |:|
Db          1 MRMLHLTLVALGAAYVCANAVESTMNRLVAETLTLLSHRTLLIGDGNLMIPTPQHTNH 60

Qy         61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
              |||:|||||||||||||:|.|.||.|:.||||||||:.|:||||:|.|||||||:::|||||
Db         61 QLCIEEVFQGIDTLKNQTAQGDAVKKIFQNLSLIKEYIDLQKRKCGGERWRVKQFLDYLQ 120

Qy        121 VFLGVINTEWTPES 134
              ||||||||||| ||
Db        121 VFLGVINTEWTES 134
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RESULT 8
ID   IL5_SHEEP      STANDARD;      PRT;   132 AA.
AC   Q28586;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
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RESULT 9
ID   Q8MKH1              PRELIMINARY;   PRT;   134 AA.
AC   Q8MKH1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Seow H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;
RT   "Cloning of ovine interleukin-5 cDNA.";
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bryson C.E., Viney E., Brandon M., Boyd A.W.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
```
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DR   EMBL; U17053; AAB60629.1; -.
DR   EMBL; U17052; AAB60629.1; JOINED.
DR   EMBL; U35038; AAC99991.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4 helix cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    132       Interleukin-5.
FT   DISULFID     61    103       Interchain (with C-103) (By similarity).
FT   DISULFID    103     61       Interchain (with C-61) (By similarity).
FT   CARBOHYD     74     74       N-linked (GlcNAc...) (By similarity).
FT   CARBOHYD     88     88       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   132 AA;  14974 MW;  D783FB720E249D9 CRC64;

Query Match             77.0%;  Score 536;  DB 1;  Length 132;
Best Local Similarity   78.8%;  Pred. No. 1.6e-44;
Matches  104;  Conservative  15;  Mismatches  13;  Indels  0;  Gaps  0;

Qy          3  MLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH   62
               ||||||||||||||||||||| |||||:|||||||||||:|||||||:|||||||||
Db          1  MHLRLTLVALGAAYVCANAVESTMNRLVAETLTLLSTHQTLLIGDGNLMIPTPQHTNHQL  60

Qy         63  CIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGEBRWRVTKFLDYLQVF  122
               ||||:||||||||||||:||:|||||||||||||||:::|||||||||||||||||||
Db         61  CIEEVFQGIDTLKNQTAQGDAVKKIFRNLSLIKEYIDLQRKCGGERWRVKQFLDYLQVF   120

Qy        123  LGVINTEWTPES  134
               ||||||||| ||
Db        121  LGVINTEWTMES  132
```

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DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin-5.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA   Heraud J.M., Lavergne A., Kazanji M.;
RT   "Molecular cloning, characterization, and quantification of squirrel
RT   monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL   Immunogenetics 54:20-29(2002).
DR   EMBL; AF294756; AAK92043.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4 helix cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin5; 1.
SQ   SEQUENCE   134 AA;  15210 MW;  EAFACCA5DB48767C CRC64;

Query Match             64.4%;  Score 448;  DB 2;  Length 134;
Best Local Similarity   67.9%;  Pred. No. 6.8e-36;
Matches  91;  Conservative  13;  Mismatches  30;  Indels  0;  Gaps  0;

Qy          1  MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH  60
               |||||:||:|||||||:| ||:|||||:|||||||||||||||:|||||||||||||||
Db          1  MRMLLHLSLLALGAAHVCANPTARPTSALVKETLAILLSTHRTLLMVNETLRIPVPAHKNH  60

Qy         61  QLCIKEVFQGIDTLKNQTAHGEAVDKCLFQNLSLIKEHIERQKKCRCAGERWRVTKFLDYLQ  120
               |||:|:||||:||||||||:|::||:|:||||||||||:||:|||||:|||||||||
Db         61  QLCTEEIFQGIGTLENQTVQGSGVEKLFQNLSLIKEHIDRQKKKCCGGERWRVKQFLDYLQ  120

Qy        121  VFLGVINTEWTPES  134
               |||||||||| ||
Db        121  EFLGVINTEWTMES  134
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RESULT 10
ID   IL5_HUMAN               STANDARD;    PRT;    134 AA.
AC   P05113; Q13840;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor) (B cell differentiation factor I).
GN   Name=IL5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87066782; PubMed=3024129;
RA   Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,
RA   Yaoita Y., Takatsu K., Hammarstroem L., Smith C.I.E., Severinson B.,
RA   Honjo T.;
RT   "Cloning of cDNA for human T-cell replacing factor (interleukin-5) and
RT   comparison with the murine homologue.";
RL   Nucleic Acids Res. 14:9149-9158(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88059042; PubMed=2824500;
RA   Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;
RT   "Molecular cloning and structure of the human interleukin-5 gene.";
RL   J. Biol. Chem. 262:16580-16584(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
```

RX   MEDLINE=88016145; PubMed=3498940;
RA   Campbell H.D., Tucker W.Q.J., Hort Y., Martinson M.E., Mayo G.,
RA   Clutterbuck E.J., Sanderson C.J., Young I.G.;
RT   "Molecular cloning, nucleotide sequence, and expression of the gene
RT   encoding human eosinophil differentiation factor (interleukin 5).";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88041112; PubMed=2823259;
RA   Yokota T., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,
RA   Yokota K., Gemmell L., Shrader B., Yang G., Meyerson P., Luh J.,
RA   Hoy P., Pene J., Briere F., Spits H., Banchereau J., de Vries J.,
RA   Lee F.D., Arai N., Arai K.;
RT   "Isolation and characterization of lymphokine cDNA clones encoding
RT   mouse and human IgA-enhancing factor and eosinophil colony-stimulating
RT   factor activities: relationship to interleukin 5.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Honjo T., Takatsu K., Severinson E.;
RL   Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 20-134, AND DISULFIDE BONDS.
RX   MEDLINE=90299868; PubMed=2361960;
RA   Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,
RA   Tsujimoto M.;
RT   "Structure of recombinant human interleukin 5 produced by Chinese
RT   hamster ovary cells.";
RL   J. Biochem. 107:292-297(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX   MEDLINE=93247642; PubMed=8483502; DOI=10.1038/363172a0;
RA   Milburn M.V., Hassell A.M., Lambert M.H., Jordan S.R.,
RA   Proudfoot A.E.I., Graber P., Wells T.N.C.;
RT   "A novel dimer configuration revealed by the crystal structure at 2.4-
RT   A resolution of human interleukin-5.";
RL   Nature 363:172-176(1993).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=91243878; PubMed=2037074; DOI=10.1016/0014-5793(91)80553-F;
RA   Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;
RT   "Human interleukin-5 expressed in Escherichia coli: assignment of the
RT   disulfide bridges of the purified unglycosylated protein.";
RL   FEBS Lett. 283:61-64(1991).

CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   -!- DATABASE: NAME=R&D Systems; cytokine mini-reviews; IL5;
CC   WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=207".

DR   EMBL; X04688; CAA28390.1; -.
DR   EMBL; J03478; AAA74469.1; -.
DR   EMBL; J02971; AAA98620.1; -.
DR   EMBL; X12705; CAA31210.1; -.
DR   EMBL; X12706; CAA31211.1; -.
DR   EMBL; AF353265; AAK19759.1; -.

DR   PIR; A28477; A28477.
DR   PDB; 1HUL; X-ray; A/B=24-131.
DR   Genew; HGNC;6016; IL5.
DR   MIM; 147850; -.
DR   PRINTS; PR004432; INTERLEUKINS.
DR   Pfam; PF02025; IL5; 1.
DR   InterPro; IPR000186; Interleukin_5.
DR   InterPro; IPR009092; 4_helix_cytokine.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; TAS.
DR   GO; GO:0009626; P:hypersensitive response; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;
KW   Growth factor; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   134   Interleukin-5.
FT   DISULFID   63   63   Interchain (with C-105).
FT   DISULFID   105   105   Interchain (with C-63).
FT   CARBOHYD   22   22   O-linked.
FT   CARBOHYD   47   47   N-linked (GlcNAc...).
FT   CONFLICT   88   88   P -> L (in Ref. 5; CAA31210).
FT   HELIX   26   38
FT   TURN   39   40
FT   HELIX   41   45
FT   TURN   46   46
FT   TURN   51   54
FT   STRAND   60   62
FT   HELIX   64   77
FT   TURN   82   82
FT   HELIX   83   103
FT   TURN   104   105
FT   STRAND   108   111
FT   HELIX   112   128
FT   TURN   129   129
SQ   SEQUENCE   134 AA; 15238 MW; DC98467179556A3 CRC64;

Query Match   61.8%; Score 430; DB 1; Length 134;
Best Local Similarity 64.9%; Pred. No. 3.9e-30;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy   1 MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKNH 60
          |||||||:||||||||||: |||: |||||||||||||||||||||||||||: |||
Db   1 MRMLLHLSLLALGAAYVVAIPTEIPTSALVKETLALLSTHRTLLTIANETLRIPVPVHKNH 60

Qy   61 QLCIKSVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEQKRKRCAGEKRRVTKFLDYLQ 120
          |||:|::|||||:|||||||||||||||||||||||||:||:||||||:||||||||||||
Db   61 QLCTEEIFQGIGTLESQTVGGGTVERLFKNLSLIKKYIDGQKKKCGEBRRRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
          ||||||||||:| ||
Db   121 EFLGVWNTEWIES 134

RESULT 11
IL5_CERTO
ID   IL5_CERTO   STANDARD;   PRT;   134 AA.
AC   P46685;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FUj;
RX   MEDLINE=96003435; PubMed=7561102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells (By
CC   similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC ---
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CC ---
DR EMBL; L26033; AAA99971.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL   1   19   By similarity.
FT CHAIN   20   134   Interleukin-5.
FT DISULFID   63   63   Interchain (with C-105) (By similarity).
FT DISULFID   105   105   Interchain (with C-63) (By similarity).
FT CARBOHYD   22   22   O-linked (By similarity).
FT CARBOHYD   47   47   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   90   90   N-linked (GlcNAc...) (Potential).
SQ SEQUENCE   134 AA; 15339 MW; 7BDD491C43798 1ED CRC64;

RESULT 12
ID   IL5_MACMU   STANDARD;   PRT;   134 AA.
AC   P48093;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

Query Match   61.6%; Score 429; DB 1; Length 134;
  Best Local Similarity   64.2%;
  Matches   86; Conservative   20; Pred. No. 4.9e-34; Mismatches 28; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAPAVENPNMRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
               |||||:|||||||:||:|| :||:|:|||||||:|:||||||||:|:| |:|:|:|||:| |
Db   1 MRMLLHLSLLALGASYMYAIPTSALVKETLTLLSTHRTLLIGNETLRIPVPVHKH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
               ||| :|:||||:|||:|| :|| ||:||:||||||||:: :::|:|| |||| |||||||
Db   61 QLCTEEIFQGIGTLESQTLQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
               ||||| ||||| ||
Db   121 BFLGVNNTEWIIES 134

RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells (By
CC   similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U19848; AAA86710.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL   1   19   By similarity.
FT CHAIN   20   134   Interleukin-5.
FT DISULFID   63   63   Interchain (with C-105) (By similarity).
FT DISULFID   105   105   Interchain (with C-63) (By similarity).
FT CARBOHYD   22   22   O-linked (By similarity).
FT CARBOHYD   47   47   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   90   90   N-linked (GlcNAc...) (Potential).
SQ SEQUENCE   134 AA; 15150 MW; DC985ECF4BAB86A3 CRC64;

RESULT 13
ID   IL5_CAVPO   STANDARD;   PRT;   135 AA.
AC   O08987;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98289181; PubMed=8764226;
RA   Mansour M., Karmilowicz M., Hawrylik S.J., Nalcerio B., Angilly J.,
RA   Conklyn M.J., Lilly C.M., Drazen J.M., Lee S.B., Auperin D.D.,
RA   de Wet J.R., Cohan V.L., Showell H.J., Danley D.E.;
RT   "Production and characterization of guinea pig IL-5 in baculovirus-

Query Match   61.2%; Score 426; DB 1; Length 134;
  Best Local Similarity   64.9%;
  Matches   87; Conservative   16; Pred. No. 9.7e-34; Mismatches 31; Indels   0; Gaps   0;

Qy   1 MRMLLNLSLLALGAAYVSAFAPAVENPNMRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
               |||||:|||||||:||:|| |||:|:|||||| || ||||||||||:| |:|:|:|||:|||
Db   1 MRMLLHLSLLALGAAVVYAIPTEIPASALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60

Qy   61 QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ 120
               ||| :|:|||| ||::|| :|| ||:||:||||||||: ::::|:|| ||||||||||||
Db   61 QLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIGGQKKKCGEERRRVNQFLDYLQ 120

Qy   121 VFLGVINTEWTPES 134
               ||||| |||||||
Db   121 BFLGVNNTEWIIES 134

RT infected insect cells.";
RL Am. J. Physiol. 270:L1002-L1007(1996).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells (By
CC   similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.

DR EMBL; U34588; AAB61357.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL   1   19   By similarity.
FT CHAIN   20   135   Interleukin-5.
FT DISULFID   64   64   Interchain (with C-106) (By similarity).
FT DISULFID   106   106   Interchain (with C-64) (By similarity).
FT CARBOHYD   48   48   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   77   77   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   91   91   N-linked (GlcNAc...) (Potential).
SQ SEQUENCE   135 AA; 15291 MW; EB85252132F52731 CRC64;

Query Match   59.6%; Score 414.5; DB 1; Length 135;
Best Local Similarity   64.9%;
Matches   87; Conservative   14; Mismatches   32; Indels   1; Gaps   1;

Qy   1 MRMLLNLSLLALGAAYVSAPAVEN-PMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKN 59
            ||||||||||||||||| || | | |||:||| |:| |||||||||||:|| |:
Db   1 MRVLLQLGLLALGAAVCVCAIPKQSATLRALVRETLTLLSTHRTLLKGNETLRISVPAHN 60

Qy   60 HQLCIKEVFQGIDTLKNQTAHGRAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYL 119
            ||||:|||||||||||||| |||||| |:|| |||||||:|:|:||| | ||||||
Db   61 HQLCIEEIFQGIDTLKNQTQGEALATLFQNLSLIKKHIDLQRQKCGEERRRVKQFLDYL 120

Qy 120 QVFLGVINTEWTPE 133
            |||||||||||| |
Db 121 QEFLAVINTEWTIE 134

ID IL5_MERUN   STANDARD;   PRT;   132 AA.
AC Q62575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name=Il5;
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Mai Z., Kiel T.R.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells (By

---

CC   similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.

DR EMBL; L37780; AAA65675.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL   1   17   Potential.
FT CHAIN   18   132   Interleukin-5.
FT DISULFID   61   61   Interchain (with C-103) (By similarity).
FT DISULFID   103   103   Interchain (with C-61) (By similarity).
FT CARBOHYD   45   45   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   74   74   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   88   88   N-linked (GlcNAc...) (Potential).
SQ SEQUENCE   132 AA; 15164 MW; 60CE3852F9F84261 CRC64;

Query Match   55.7%; Score 388; DB 1; Length 132;
Best Local Similarity   59.4%;
Matches   79; Conservative   21; Mismatches   31; Indels   2; Gaps   1;

Qy   1 MRMLLNLSLLALGAAYVSAPAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNH 60
            ||:| |:|:| || |:|:|| | | |:| |||||||||||||:||:|||||| |:
Db   1 MRLPLQLSILTL--AWVWAVALEIPMSAVVKETLIQLSTHRALLTSNETVRLPVPTHKNH 58

Qy   61 QLCIKEVFQGIDTLKNQTAHGRAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQ 120
           |||:||||||||:||||| |||:|| ||||||||:|||:|:|:|||| | |||||||
Db   59 QLCIGEIFQLDILKNQTARGGAVETLFQNLSLIKKYIDRQKEKCGEERRARQFLDYLQ 118

Qy 121 VFLGVINTEWTPE 133
            |||||||||||
Db 119 EFLGVMSTEWTME 131

ID IL5_SIGHI   STANDARD;   PRT;   132 AA.
AC Q9ESI9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN Name=Il5;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX PubMed=11054577; DOI=10.1016/S0378-1119(00)00366-8;
RA Howard S., Jacquet A., Haumont M., Daminet V., Milican F., Glineur F.,
RA Bollen A.;
RT "Cloning, expression and purification of recombinant cotton rat
RT interleukin-5.";
RL Gene 257:149-155(2000).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells.

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CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   ------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------
DR   EMBL; AF148211; AAG16722.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     19       By similarity.
FT   CHAIN        20    132       Interleukin-5.
FT   DISULFID     61    103       Interchain (with C-103) (By similarity).
FT   DISULFID    103     61       Interchain (with C-61) (By similarity).
FT   CARBOHYD     45     45       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     74     74       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     88     88       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   132 AA;  15434 MW;  B328B81B2371FEB9 CRC64;
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Query Match        55.7%;     Score 388;   DB 1;   Length 132;
Best Local Similarity  59.4%;  Pred. No. 5e-30;
Matches   79;  Conservative  19;  Mismatches  33;  Indels  2;  Gaps  1;

Qy     1  MRMLLNLSLLALGAAYVSAFAVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNH  60
          |||||||:||||:|::|||||::|||::  ||:|||||||:::|::||:|||||||:||:|
Db     1  MRMLLHLSILJTL--ACVWTFAVEIPMHTVVKETLIQLSTHRALLTSNETVRLPVPTHKNH  58

Qy    61  QLCIKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQ  120
          |||| |:|:|:|  ||||||::|:|::|||||:::|:|:||:::|  |||  |||||||
Db    59  QLCIGEIFRGLDILKNQTVRGGTVETLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQ  118

Qy   121  VFLGVINTEWTPE  133
          |||||:||||||
Db   119  EFLGVMGTEWTME  131
```

Search completed: August 4, 2005, 17:11:05
Job time : 126.622 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: August 4, 2005, 16:50:05 ; Search time 115.462 Seconds
           (without alignments)
           385.213 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVABTLTLLST.........FLDYLQVFLGVINTEWTPES 115

Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 100 summaries

Database :   A_Geneseq_16Dec04:*
         1: geneseqp1980s:*
         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	610	100.0	115	3	AAY58220	Canine ma
2	610	100.0	134	3	AAY58219	Canine in
3	601	98.5	134	4	AAB72615	Canine in
4	487	79.8	132	2	AAW08479	Ovine IL-
5	358	58.7	115	1	ADL89254	Human mod
6	357	58.5	113	1	ADK17208	Sequence
7	357	58.5	115	8	AAP93152	Sequence
8	357	58.5	287	6	ADL89235	Human mod
9	356	58.4	112	1	AAO30459	Human mod
10	356	58.4	115	1	AAP80279	Pleiotrop
11	356	58.4	115	3	AAB45489	Human mod
12	356	58.4	115	1	AAP81038	Sequence
13	356	58.4	115	2	ABG94295	Human mat
14	356	58.4	115	5	ABG80607	Human mat
15	356	58.4	115	7	AAO30453	Human mod
16	356	58.4	115	8	ADK17208	Human int
17	356	58.4	115	8	ADL89261	Human mod
18	356	58.4	115	8	ADL88874	Human cyt
19	356	58.4	115	8	ADL88240	Human mod
20	356	58.4	115	8	ADL89246	Human mod
21	356	58.4	115	8	ADL89255	Human mod
22	356	58.4	115	5	ABG94353	Human C-I
23	356	58.4	115	5	ABG80665	Human C-I
24	356	58.4	123	7	ADK17224	Human C-I
25	356	58.4	134	2	AAR92802	Human int
26	356	58.4	134	4	AAB72617	Human int
27	356	58.4	134	2	ABG94294	Human int
28	356	58.4	134	5	ABG80606	Human pre
29	356	58.4	134	8	AAU10353	Interleuk
30	356	58.4	134	7	ADF70849	Human int
31	356	58.4	134	7	ADK17207	Human int
32	356	58.4	134	8	ADP56010	Human PRO
33	356	58.4	136	7	ABG94352	Human C-I
34	356	58.4	136	5	ABG80664	Human C-I
35	356	58.4	136	7	ADK17223	Human C-I
36	356	58.4	138	2	ABG94351	Human ILn
37	356	58.4	138	5	ABG80663	Human ILn
38	356	58.4	138	7	ADK17222	Human C-I
39	356	58.4	356	6	ADL89262	Human mod
40	356	58.4	356	6	AAO30460	hIL5.37 v
41	356	58.4	287	6	AAO30457	hIL5-P2-P
42	356	58.4	285	6	AAO30458	hIL5-P30-
43	355	58.2	285	6	ADL89251	Human mod
44	355	58.2	355	8	ADL89247	Human mod
45	355	58.2	355	6	ADL89241	Human mod
46	355	58.2	355	6	ADL89234	Human mod
47	355	58.2	355	8	ADL89263	Human mod
48	354	58.0	355	8	ADL89248	Human mod
49	354	58.0	354	8	ADL89252	Human mod
50	354	58.0	354	8	ADL89242	Human mod
51	353	57.9	353	8	ADL89243	Human mod
52	353	57.9	353	8	ADL89256	Human mod
53	352	57.7	353	8	ADL89264	Human mod
54	352	57.7	352	8	ADL89260	Human mod
55	352	57.7	352	8	ADL89249	Human mod
56	352	57.7	352	5	ADL89238	Human mod
57	351	57.5	134	5	AAU10354	Interleuk
58	351	57.5	351	8	ADL89239	Human mod
59	351	57.5	351	8	ADL89250	Human mod
60	351	57.5	351	8	ADL89259	Human mod
61	351	57.5	351	8	ADL89245	Human mod
62	351	57.5	351	8	ADL89244	Human mod
63	351	57.5	351	8	ADL89258	Human mod
64	351	57.5	351	8	ADL89257	Human mod
65	351	57.5	351	8	ADL89266	Human mod
66	351	57.5	351	8	ADL89265	Human mod
67	351	57.5	121	2	AAW43436	Human int
68	348	57.0	348	8	ADL89236	Human mod
69	348	57.0	348	8	ADL89237	Human mod
70	347	56.9	347	2	AAW05273	N-termina
71	347	56.9	115	2	AAW72948	Truncated
72	347	56.9	347	1	AAP71064	Murine eo
73	347	56.9	347	1	AAP82969	B cell di
74	347	56.9	347	2	AAR96963	T cell re
75	347	56.9	347	2	AAW72949	T cell re
76	347	56.9	347	2	AAW72947	T cell re
77	347	56.9	347	4	AAB72618	Murine in
78	347	56.9	347	5	ABG94349	Human C-I
79	347	56.9	347	5	ABG80661	Human IL-
80	346	56.7	346	7	ADK17220	Human IL-
81	344	56.4	344	1	AAP81056	Human C-I
82	344	56.4	344	5	ABG94348	Mouse C-I
83	344	56.4	344	5	ABG80660	Mouse IL-
84	344	56.4	344	7	ADK17219	Mouse C-I
85	343	56.2	84	4	AAB72616	Canine in
86	343	56.2	343	2	AAW05274	N-termina
87	343	56.2	343	5	ABG94296	Mouse mat
88	343	56.2	343	5	ABG80608	Mouse int
89	343	56.2	343	7	ADK17209	Mouse int
90	343	56.2	343	5	ADL89268	Human mod
91	343	56.2	343	2	ABG94350	Mouse C-I
92	343	56.2	343	5	ABG80662	Mouse IL-
93	342	56.1	342	7	ADK17221	Mouse C-I
94	342	56.1	342	2	AAW05275	N-termina
95	339	55.6	342	8	ADL89267	Human mod
96	339	55.6	339	2	ABG94353	Human IL-
97	335	54.9	335	3	ADK17224	Human C-I
98	332.5	54.5	126	3	AAB45490	Modified

RESULT 1

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ID    AAY58220 standard; protein; 115 AA.
XX
AC    AAY58220;
XX
DT    14-MAR-2000  (first entry)
XX
DE    Canine mature interleukin-5 (IL-5).
XX
KW    Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW    immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS    Canis familiaris.
XX
PN    WO9961618-A2.
XX
PD    02-DEC-1999.
XX
PF    28-MAY-1999;   99WO-US011942.
XX
PR    29-MAY-1998;   98US-0087306P.
XX
PA    (HESK-) HESKA CORP.
XX
PI    Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR    WPI; 2000-072623/06.
DR    N-PSDB; AAZ55550, AAZ55551.
XX
PT    Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT    useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS    Claim 3h; Page 227; 264pp; English.
XX
CC    Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
CC    -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3
CC    ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
CC    canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
CC    granulocyte macrophage colony-stimulating factor (GMCSF), and nucleotides
CC    which encode these immunoregulatory proteins. The proteins, their
CC    associated nucleic acids, specific antibodies and inhibitors may be used
CC    as vaccines for therapeutic or prophylactic regulation of an immune
CC    response in animals (particularly cats, dogs, horses and humans). They
CC    may be used to treat autoimmune or infectious diseases including
CC    allergies, tumours, inflammation and graft rejection, and to increase the
CC    response from a co-administered antigen. The nucleotide sequences can
CC    also be used for the recombinant production of a protein, while
CC    nucleotide fragments are useful as probes, as amplification primers and
CC    as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC    The proteins may be used to raise antibodies and to screen for modulators
CC    of activity, while the antibodies may be used in detection, and in drug
CC    targeting
XX
SQ    Sequence 115 AA;
```

```
Query Match             100.0%;  Score 610;  DB 3;  Length 115;
Best Local Similarity   100.0%;  Pred. No. 2.6e-64;
Matches  115;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy           1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy          61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
```

RESULT 2

```
ID    AAY58219 standard; protein; 134 AA.
XX
AC    AAY58219;
XX
DT    14-MAR-2000  (first entry)
XX
DE    Canine interleukin-5 (IL-5).
XX
KW    Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW    immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS    Canis familiaris.
XX
PN    WO9961618-A2.
XX
PD    02-DEC-1999.
XX
PF    28-MAY-1999;   99WO-US011942.
XX
PR    29-MAY-1998;   98US-0087306P.
XX
PA    (HESK-) HESKA CORP.
XX
PI    Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR    WPI; 2000-072623/06.
DR    N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.
XX
PT    Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT    useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS    Claim 3h; Page 224; 264pp; English.
XX
CC    Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
CC    -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3
CC    ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
CC    canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
CC    granulocyte macrophage colony-stimulating factor (GMCSF), and nucleotides
CC    which encode these immunoregulatory proteins. The proteins, their
CC    associated nucleic acids, specific antibodies and inhibitors may be used
CC    as vaccines for therapeutic or prophylactic regulation of an immune
CC    response in animals (particularly cats, dogs, horses and humans). They
CC    may be used to treat autoimmune or infectious diseases including
CC    allergies, tumours, inflammation and graft rejection, and to increase the
CC    response from a co-administered antigen. The nucleotide sequences can
CC    also be used for the recombinant production of a protein, while
CC    nucleotide fragments are useful as probes, as amplification primers and
CC    as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC    The proteins may be used to raise antibodies and to screen for modulators
CC    of activity, while the antibodies may be used in detection, and in drug
CC    targeting
XX
SQ    Sequence 134 AA;
```

```
Query Match             100.0%;  Score 610;  DB 3;  Length 134;
Best Local Similarity   100.0%;  Pred. No. 3.2e-64;
Matches  115;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy           1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy          61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          80 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
```

RESULT 3

```
RESULT 1
```

ALIGNMENTS

```
99    332.5   54.5   126   3   AAB45514        Aab45514 Modified
100   331.5   54.3   132   3   AAB45520        Aab45520 Modified

Db          61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
```

```
ID   AAB72615 standard; protein; 134 AA.
XX
AC   AAB72615;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Canine interleukin-5 protein #1.
XX
KW   Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW   inflammatory reaction.
XX
OS   Canis sp.
XX
XX
PN   WO200111049-A2.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000; 2000WO-US021651.
XX
PR   10-AUG-1999; 99US-0371615.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Guo H, Lawton R, Mermer B, Aiyappa AP;
XX
DR   WPI; 2001-191542/19.
DR   N-PSDB; AAF74300.
XX
PT   Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT   generating antibodies which are useful in treating allergies in dogs.
XX
PS   Claim 29; Page 46-47; 48pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC   cancer and inflammatory reactions in dogs. The present sequence is one
CC   version of the IL-5 protein shown in the specification
XX
SQ   Sequence 134 AA;

Query Match             98.5%;  Score 601; DB 4;  Length 134;
Best Local Similarity   99.1%;
Matches  114;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy         61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              ||||||||||||||||||||||||||||||||||||||||||||| ||
Db         80 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTMES 134
```

```
RESULT 4
ID   AAW08479 standard; protein; 132 AA.
XX
AC   AAW08479;
XX
DT   17-OCT-2003  (revised)
DT   24-SEP-1997  (first entry)
XX
DE   Ovine IL-5.
XX
KW   Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW   livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW   immunosuppression; allergy; reproductive system; growth; early maturity;
KW   antibody; diagnosis; immunopotentiator;
KW   early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW   secretion; IgM; IgA; bacterial endotoxin; gamma-interferon.
XX
OS   Ovis aries.
XX
```

```
XX
PN   WO9700321-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;  96WO-AU000360.
XX
PR   14-JUN-1995;  95AU-00003502.
PR   27-OCT-1995;  95AU-00006244.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Seow H, Wood P;
XX
DR   WPI; 1997-077528/07.
DR   N-PSDB; AAT50755, AAT50756.
XX
PT   This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5
PT   or IL-12 are used to treat and/or prevent infections in livestock (esp.
CC   cows and sheep), particularly where the animals are stressed, e.g. during
CC   transport. IL-5, and IL-12 can also be used as adjuvants in vaccines for
CC   veterinary use (partic. weakly immunogenic subunit or synthetic peptide
CC   vaccines). They may also be used to treat cancer, immunosuppression and
CC   allergy, to enhance/suppress the reproductive system and to promote
CC   growth or early maturity. Optionally interleukin can be delivered from
CC   constructs or delivery cells and antibodies are useful in enzyme
CC   immunoassays for rapid diagnosis of infection. The interleukins are
CC   immunopotentiators, especially IL-5 promotes growth of early
CC   haematopoietic progenitor cells and generation of cytotoxic cells from
CC   thymocytes, also it stimulates production and secretion of IgM and IgA
CC   (in synergism with bacterial endotoxin). IL-12 induces production of
CC   gamma-interferon by, and proliferation of, T and NK cells and increases
CC   the (non-)specific cytolytic lymphocyte response. The genetic constructs
CC   can also be used for in vitro production of IL-5 or -12. (Updated on 17-
CC   OCT-2003 to standardise OS field)
XX
SQ   Sequence 132 AA;

Query Match             79.8%;  Score 487; DB 2;  Length 132;
Best Local Similarity   80.7%;
Matches   92;  Conservative  13;  Mismatches   9;  Indels   0;  Gaps   0;

Qy          2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAH 61
              ||||.|||||||||||||||||||||||||||.||:|:||||||||||||||||||||||
Db         19 AVESTMNRLVAETLTLLSTHQTLLIGDGNLMIPTPQHTNHQLCIEEVFQGIDTLKNQTAQ 78

Qy         62 GEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |||:|||||||||||||||||||||||||||||:|:||||||||||||||||||||
Db         79 GDAVKKIFRNLSLIKEYIDLQKRKCGGERWRVKQFLDYLQVFLGVINTEWTMES 132
```

```
RESULT 5
ID   ADL89254 standard; protein; 115 AA.
XX
AC   ADL89254;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human modified cytokine protein #536.
XX
KW   Human; cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10;
KW   long-chain cytokine family; short-chain cytokine family; infection;
KW   allergy; heart disease; cancer; liver disorder; autoimmune disease;
KW   growth disorder; diabetes; neurodegenerative disease; antimicrobial;
KW   antiallergic; cytostatic; immunosuppressive; antidiabetic;
KW   neuroprotective; mutant; mutein.
XX
```

OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004022593-A2.
XX
PD   18-MAR-2004.
XX
PF   08-SEP-2003; 2003WO-IB004347.
XX
PR   09-SEP-2002; 2002US-0409898P.
PR   21-MAR-2003; 2003US-0457135P.
XX
PA   (NAUT-) NAUTILUS BIOTECH.
XX
PI   Gantier R, Guyon T, Vega M, Drittanti L;
XX
DR   WPI; 2004-248447/23.
XX
PT   New modified cytokines with increased resistance to proteolysis, useful
PT   for diagnosing and treating diseases such as infections, allergies, heart
PT   diseases, cancer, liver disorders, autoimmune diseases or diabetes.
XX
PS   Disclosure; SEQ ID NO 588; 316pp; English.
XX
CC   The invention relates to modified cytokines that exhibit increased
CC   resistance to proteolysis compared to unmodified cytokines. The invention
CC   also relates to nucleic acid molecules encoding the cytokines, a
CC   pharmaceutical composition comprising a nucleic acid molecule in a
CC   pharmaceutical carrier, and a method of generating a protein or peptide
CC   molecule having a predetermined property or activity, or a pre-selected
CC   altered phenotype. The modified cytokine is selected from a member of the
CC   interferons (IFNs)/interleukin (IL)-10 protein family, a member of the
CC   interleukin (IL) protein family or a member of the short-chain cytokine
CC   family. The composition and method are useful for diagnosing and treating
CC   diseases such as infections, allergies, heart diseases, cancer, liver
CC   disorders, autoimmune diseases, growth disorders, diabetes or
CC   neurodegenerative diseases. This sequence represents a human modified
CC   cytokine protein of the invention.
XX
SQ   Sequence 115 AA;

Query Match   58.7%; Score 358; DB 8; Length 115;
Best Local Similarity   62.5%; Pred. No. 2.7e-34;
Matches   70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGB 63
              ||||||||| |||||||||||:|||||||||||||||||||||: :|| ||||||||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKRNQLCTEEIFQGIGTLESQTVCGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |:||:||:|:||||||:||:||::|||||||||||||||||:|||||:||
Db   64 TVERLFKNLSLIKKYIDGQKKKCGNERRRVNQFLDYLQEFLGVWNTEWIIES 115

RESULT 6
AAP93152
ID   AAP93152 standard; protein; 113 AA.
XX
AC   AAP93152;
XX
DT   15-MAR-1992 (first entry)
XX
DE   Sequence of human interleukin-5 (IL-5).
XX
KW   B-cell growth factor; lymphokine; B-cell stimulating factor 2.
XX
OS   Homo sapiens.
XX
PN   GB2217328-A.
XX
PD   25-OCT-1989.
XX
PF   12-APR-1988; 88GB-00008524.
PP   12-APR-1988; 88GB-00008524.

XX
PR   12-APR-1988; 88GB-00008524.
XX
PA   (BRBI-) BRITISH BIO-TECH L.
XX
PI   Edwards RM;
XX
DR   WPI; 1989-311767/43.
DR   N-PSDB; AAN91647.
XX
PT   Synthetic gene encoding human interleukin-5 - has restriction sites at
PT   frequent intervals to facilitate manipulation.
XX
PS   Disclosure; Fig 3a; 21pp; English.
XX
CC   AAN91647 has restriction sites for HindIII, BspMI, NcoI, SpeI, BspMII,
CC   ApaLI, XmnI, ClaI, BalI, PstI, DraIII, BamHI and EcoRI. IL5 acts as a B-
CC   cell growth and differentiation factor
XX
SQ   Sequence 113 AA;

Query Match   58.5%; Score 357; DB 1; Length 113;
Best Local Similarity   61.9%; Pred. No. 3.5e-34;
Matches   70; Conservative 17; Mismatches 26; Indels   0; Gaps   0;

Qy   3 VENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHG 62
              :|| :|| |||||||||||||||||||||||||||||||||:: :|| |||||||||
Db   1 MEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKRNQLCTEEIFQGIGTLESQTVCGG 60

Qy   63 EAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |:||||:||:|:||||||:||:||::|||||||||||||||||:|||||:||
Db   61 GTVERLFKNLSLIKKYIDGQKKKCGNERRRVNQFLDYLQEFLGVWNTEWIIES 113

RESULT 7
ADL89235
ID   ADL89235 standard; protein; 115 AA.
XX
AC   ADL89235;
XX
DT   03-JUN-2004 (first entry)
XX
DE   Human modified cytokine protein #517.
XX
KW   Human; cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10;
KW   long-chain cytokine family; short-chain cytokine family; infection;
KW   allergy; heart disease; cancer; liver disorder; autoimmune disease;
KW   growth disorder; diabetes; neurodegenerative disease; antimicrobial;
KW   antiallergic; cytostatic; immunosuppressive; antidiabetic;
KW   neuroprotective; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004022593-A2.
XX
PD   18-MAR-2004.
XX
PF   08-SEP-2003; 2003WO-IB004347.
XX
PR   09-SEP-2002; 2002US-0409898P.
PR   21-MAR-2003; 2003US-0457135P.
XX
PA   (NAUT-) NAUTILUS BIOTECH.
XX
PI   Gantier R, Guyon T, Vega M, Drittanti L;
XX
DR   WPI; 2004-248447/23.
XX
PT   New modified cytokines with increased resistance to proteolysis, useful
PT   for diagnosing and treating diseases such as infections, allergies, heart
PT   diseases, cancer, liver disorders, autoimmune diseases or diabetes.
XX

```
PS   Disclosure; SEQ ID NO 569; 316pp; English.
XX
CC   The invention relates to modified cytokines that exhibit increased
CC   resistance to proteolysis compared to unmodified cytokines. The invention
CC   also relates to nucleic acid molecules encoding the cytokines, a
CC   pharmaceutical composition comprising a nucleic acid molecule in a
CC   pharmaceutical carrier, and a method of generating a protein or peptide
CC   molecule having a predetermined property or activity, or a pre-selected
CC   altered phenotype. The modified cytokine is selected from a member of the
CC   interferons (IFNs)/interleukin (IL)-10 protein family, a member of the
CC   long-chain cytokine family or a member of the short-chain cytokine
CC   family. The composition and method are useful for diagnosing and treating
CC   disorders such as infections, allergies, heart diseases, cancer, liver
CC   disorders, autoimmune diseases, growth disorders, diabetes or
CC   neurodegenerative diseases. This sequence represents a human modified
CC   cytokine protein of the invention.
XX
SQ   Sequence 115 AA;

Query Match        58.5%;  Score 357; DB 8; Length 115;
Best Local Similarity   62.5%; Pred. No. 3.6e-34;
Matches   70; Conservative  16; Mismatches  26; Indels   0; Gaps   0;

Qy   4  ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNNHQLCIKEVPQGIDTLKNQTAHGE 63
          |::||| |||| ||: ||:|||||||  ||| || :||||||| ||| ||| ||  |
Db   4  EBIPTSALVKETLALLSTHRTLLIANETLQIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

Qy  64  AVDKLFQNLSLIKEHIEROKKRCRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
          :||| |||||||||  || | |||||||||||  | :| ||||||||||||||
Db  64  TVERLFKNLSLIKKYIDGQKKKCGEBERRRVNQFLDYLQEFLGVMNTEWIIES 115


RESULT 8
ID   AAO30459  standard; protein; 287 AA.
XX
AC   AAO30459;
XX
DT   22-SEP-2003  (first entry)
XX
DE   hIL5.36 variant protein.
XX
KW   Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW   tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
KW   IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "Human hIL5.36 leader peptide"
FT   Protein         20..287
FT                   /note= "Mature hIL5.36 protein"
FT   Region          24..44
FT                   /note= "Tetanus toxoid P30 epitope"
FT   Region          273..287
FT                   /note= "Tetanus toxoid P2 epitope"
XX
PN   WO200304224-A2.
XX
PD   22-MAY-2003.
XX
PF   15-NOV-2002; 2002WO-DK000764.
XX
PR   16-NOV-2001; 2001DK-00001702.
PR   16-NOV-2001; 2001US-0331575P.
XX
PA   (PHAR-) PHARMEXA AS.
PA   (KLYS/) KLYSNER S.
PA   (NIEL/) NIELSEN F S.
PA   (BRAT/) BRATT T.
PA   (VOLD/) VOLDBORG B.
PA   (MOUR/) MOURITSEN S.
XX
PI   Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX
DR   WPI; 2003-449558/42.
DR   N-PSDB; AAL61295.
XX

New immunogenic analogue of a polymeric protein, useful for preparing a
composition for treating inflammatory diseases e.g. arthritis.

PS   Claim 20; Page 115-117; 196pp; English.
XX
CC   The invention relates to immunogenic analogues of multimeric proteins
CC   such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC   factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC   analogues. The immunogenic analogue is useful for preparing a composition
CC   for treating inflammatory diseases, e.g., arthritis. It is also used in
CC   gene therapy. The present sequence is a fusion construct variant which
CC   comprises 2 human interleukin 5 (IL5) monomers joined by diglycine linker
CC   and including terminally positioned tetanus toxoid epitopes P30 and P2.
CC   This sequence is used to illustrate the method of the invention
XX
SQ   Sequence 287 AA;

Query Match        58.5%;  Score 357; DB 6; Length 287;
Best Local Similarity   61.9%; Pred. No. 1.3e-33;
Matches   70; Conservative  17; Mismatches  26; Indels   0; Gaps   0;

Qy   3  VENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNNHQLCIKEVPQGIDTLKNQTAHG 62
          : | || |||| ||||| ||:|||||||  ||| || :|||| |||| ||| || ||  |
Db  43  LEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 102

Qy  63  EAVDKLFQNLSLIKEHIEROKKRCRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
          :||| |||||||||  ||| | |||||||||  | :| ||||||||||||||
Db 103  GTVERLFKNLSLIKKYIDGQKKKCGEBERRRVNQFLDYLQEFLGVMNTEWIIES 155


RESULT 9
ID   AAP80279  standard; protein; 112 AA.
XX
AC   AAP80279;
XX
DT   25-MAR-2003  (revised)
DT   20-NOV-1990  (first entry)
XX
DE   Pleiotropic immune factor (PIF).
XX
KW   Pleiotropic immune factor; PIF; immune system mediator; IgA;
KW   immunoglobulin secretion; eosinophil-colony stimulating factor;
KW   B-cell differentiation factor.
XX
OS   Homo sapiens.
XX
DE   EP267779-A.
XX
PN   10-NOV-1987;  87EP-00309935.
XX
PD   18-MAY-1988.
XX
PR   10-NOV-1986;  86US-00928900.
PR   05-JAN-1987;  87US-00000551.
XX
PA   (SCHE ) SCHERING BIOTECH CORP.
XX
PI   Coffman R, Yokota T, Crute JJ, Lee F, Arai K;
XX
DR   WPI; 1988-134622/20.
XX
PT   New human pleiotropic immune factor and mutant forms - for stimulating
PT   immunoglobulin prodn. and new DNA coding sequences.
XX
```

PS Claim 4; Page 26; 39pp; English.
XX
CC The peptide has eosinophil colony stimulating factor activity (EoCSF)
CC and/or B cell differentiation factor activity. It can be used to
CC stimulate prodn. of immunoglobulins, esp. IgA, for treating respiratory
CC and gastrointestinal infections.The protein is produced by recombinant
CC DNA techniques using mRNA from cells showing EoCSP activity (ATCC CRL
CC 8179). The cloned DNA can also be engineered to express mutants with
CC improved properties. See also AAP80280. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 112 AA;

Qy Query Match   58.4%; Score 356; DB 1; Length 112;
Best Local Similarity   62.5%; Pred. No. 4.5e-34;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         |:| |||||||||| ||||||||| : ||||||||||||||| ||:||||:|:|
Db   1 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEIFQGIGTLESQTVCGG 60

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         |:||||||||||:|:|: |||:| ||||||| ||||||| ||
Db   61 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQEFLGVWNTEWIES 112

RESULT 10
ID AAP81038 standard; protein; 115 AA.
XX
AC AAP81038;
XX
DT 25-MAR-2003 (revised)
DT 04-DEC-1990 (first entry)
XX
DE Sequence of human B-cell differentiation factor.
XX
KW Immunodeficiency disease; cancer therapy; interleukin; lymphocyte.
XX
OS Homo sapiens.
XX
PN EP261625-A.
XX
PD 30-MAR-1988.
XX
PF 21-SEP-1987; 87EP-00113774.
PR 20-SEP-1986; 86JP-00223284.
PR 21-SEP-1987; 87JP-00236842.
XX
PA (HONJ/) HONJO T.
XX
PI Honjo T, Takatu K, Severinson B;
XX
DR WPI; 1988-085927/13.
XX
PT Recombinant human B-cell differentiation factor - used for diagnosis or
PT treatment of immuno:deficiency diseases, various infections and cancers.
XX
PS Claim 8; Page 17; 5pp; English.
XX
CC BCDF has an approx. molecular weight of 13,149. The BCDF is useful in the
CC diagnosis or treatment of e.g. immunodeficiency diseases which occur due
CC to the deficiency of this factor in a living body and also in the
CC treatment of various infections and cancers. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 115 AA;

Qy Query Match   58.4%; Score 356; DB 1; Length 115;
Best Local Similarity   62.5%; Pred. No. 4.7e-34;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         |:| |||||||||| ||||||||| : ||||||||||||||| ||:||||:|:|
Db   1 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEIFQGIGTLESQTVCGG 60

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         |:||||||||||:|:|: |||:| ||||||| ||||||| ||
Db   61 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQEFLGVWNTEWIES 112

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         |:| |||||||||| ||||||||| : ||||||||||||||| ||:||||:|:|
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEIFQGIGTLESQTVCGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         |:||||||||||:|:|: |||:| ||||||| ||||||| ||
Db   64 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQEFLGVWNTEWIES 115

RESULT 11
ID AAB45489 standard; protein; 115 AA.
XX
AC AAB45489;
XX
DT 26-FEB-2001 (first entry)
XX
DE Human interleukin-5 mature protein SEQ ID NO: 1.
XX
KW Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;
KW cancer; eosinophilia; vaccine; allergic rhinitis.
XX
OS Homo sapiens.
XX
PN WO200065058-A1.
XX
PD 02-NOV-2000.
XX
PF 19-APR-2000; 2000WO-DK000205.
XX
PR 23-APR-1999; 99DK-00000552.
PR 06-MAY-1999; 99US-0132811P.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Klysner S;
XX
DR WPI; 2000-672791/65.
XX
PT Down-regulating interleukin 5 (IL-5) activity in humans by administering
PT IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or
PT amelioration of asthma or other chronic allergic conditions.
XX
PS Claim 19; Page 118; 172pp; English.
XX
CC The present invention is concerned with methods of treating asthma,
CC eosinophilia, allergic rhinitis and other allergic diseases. These
CC involve the use of interleukin-5 (IL-5) analogues and modified IL-5
CC proteins and their coding sequences to down-regulate IL-5 activity and
CC thus reduce eosinophil numbers. The allergic diseases may be treated
CC using autovaccines, nucleic acid vaccines or live vaccines. In addition,
CC it is possible that they may be used in the treatment of cancer and
CC helminthic infections
XX
SQ Sequence 115 AA;

Qy Query Match   58.4%; Score 356; DB 3; Length 115;
Best Local Similarity   62.5%; Pred. No. 4.7e-34;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         |:| |||||||||| ||||||||| : ||||||||||||||| ||:||||:|:|
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEIFQGIGTLESQTVCGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         |:||||||||||:|:|: |||:| ||||||| ||||||| ||
Db   64 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQEFLGVWNTEWIES 115

RESULT 12
ID ABG94295 standard; protein; 115 AA.
XX

AC   ABG94295;
XX
DT   10-DEC-2002 (first entry)
XX
DE   Human mature interleukin 5 protein.
XX
KW   Human; mouse; rat; antimicrobial; antiviral; antiallergic; immunomodulatory;
KW   cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW   vaccine; infectious disease.
XX
OS   Homo sapiens.
XX
XX
PN   WO20025690S-A2.
XX
PD   25-JUL-2002.
XX
DR   WPI; 2002-627751/67.
PI   Renner WA, Bachmann M, Tissot A, Maurer P, Lechner P, Sebbel P;
PI   Piossek C;
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PF   21-JAN-2002; 2002WO-IB000166.
XX
PR   19-JAN-2001; 2001US-0262379P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-0326998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 422; 441pp; English.
XX
CC   This invention relates to a novel ordered and repetitive antigen array
CC   used in the production of vaccines for infectious diseases. The invention
CC   also discloses a composition comprising a non-natural molecular scaffold
CC   comprising a core particle selected from a core particle of a non-natural
CC   origin and a core particle of natural origin and an organiser comprising
CC   at least one first attachment site, where the organiser is connected to
CC   the core particle by at least one covalent bond. Also disclosed is an
CC   antigen or antigenic determinant with at least one second attachment
CC   site, where the antigen or antigenic determinant is amyloid beta peptide
CC   (Abeta1-42) or its fragment and where the second attachment site is
CC   selected from an attachment site not naturally occurring with the antigen
CC   or antigenic determinant and an attachment site naturally occurring with
CC   the antigen or antigenic determinant, where the second attachment site is
CC   capable of association through at least one non-peptide bond to the first
CC   attachment site and where the antigen or antigenic determinant and the
CC   scaffold interact through the association to form an ordered and
CC   repetitive antigen array. The invention also comprises a coat protein
CC   capable of forming a capsid which comprises mutant Qbeta coat proteins
CC   having an amino acid sequence selected from five amino acid sequences
CC   fully defined in the specification. The compounds of the invention may
CC   have antimicrobial, antidiabetic, antiallergic, immunomodulatory,
CC   antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC   immunisation and as a vaccine. The present sequence represents a protein
CC   sequence used to create the compositions of the invention
XX
SQ   Sequence 115 AA;
XX

Query Match   58.4%; Score 356; DB 5; Length 115;
Best Local Similarity   62.5%; Pred. No. 4.7e-34;
Matches   70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

```
Qy          4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
                : ||| ||| |||:|| ||:||| :||||:|| | :|||||  |||||:|| :|
Db          4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEBIFQGITLBSQTVQGG 63

Qy         64 AVDKLFQNLSLIKHIERQKRCAGERWRVTKFPLDYLQVPLGVINTEWTPES 115
                |:|||||||||:||||||| ||:| |:| ||||:|||||||||||||||
Db         64 TVERLFKNLSLIKYIDGQKKCGEERRVNQFDLYLQBFLGVMNTEWIIBS 115
```

RESULT 13
ABG80607
ID   ABG80607 standard; protein; 115 AA.
XX
AC   ABG80607;
XX
DT   29-NOV-2002 (first entry)
XX
DE   Human mature Interleukin 5.
XX
KW   Molecular antigen array; vaccine; antigen; antimicrobial;
KW   molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW   graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW   adult respiratory distress syndrome; ARDS; Crohn's disease;
KW   allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW   Grave's disease; systemic lupus erythematosus; osteoporosis;
KW   inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW   immunoproliferative disease lymphadenopathy; Alzheimer's disease;
KW   angioimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy;
KW   rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW   enterokinase; cysteine-containing linker.
XX
OS   Homo sapiens.
XX
XX
PN   WO200256907-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000168.
XX
PR   19-JAN-2001; 2001US-0262379P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-0326998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
DR   WPI; 2002-636514/68.
PI   Maurer P, Lechner P, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI   Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (NOVS-) NOVARTIS PHARMA AG.
PA   (MAUR/) MAURER P.
PA   (LECH/) LECHNER P.
PA   (ORTM/) ORTMANN R.
PA   (LUEO/) LUEOEND R.
PA   (STAU/) STAUFENBIEL M.
PA   (FREY/) FREY P.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 399; 418pp; English.
XX
CC   The invention relates to a composition comprising: (a) a non-natural
CC   molecular scaffold comprising: (1) a core particle selected from: (1) a
CC   core particle of a non-natural origin; and (2) a core particle of natural
CC   origin; and (ii) an organiser comprising at least one first attachment
CC   site, where the organiser is connected to the core particle by at least
CC   one covalent bond; (b) an antigen or antigenic determinant with at least
CC   one second attachment site, where the antigen or antigenic determinant is
CC   amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC   attachment site is selected from: (i) an attachment site not naturally
CC   occurring with the antigen or antigenic determinant; and (ii) an
CC   attachment site naturally occurring with the antigen or antigenic
CC   determinant, where the second attachment site is capable of association
CC   through at least one non-peptide bond to the first attachment site; and
CC   where the antigen or antigenic determinant and the scaffold interact
CC   through the association to form an ordered and repetitive antigen array.
CC   Also included is a process for producing a non-naturally occurring
CC   ordered and repetitive antigen array. The composition is used in

CC   immunisation and as a vaccine for diseases such as influenza, graft
CC   versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
CC   respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC   acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC   systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC   gravis, immunoproliferative disease lymphadenopathy,
CC   angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC   rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC   osteoporosis and infectious diseases. The present sequence is an antigen
CC   for use in the array of the invention. The antigen is modified to posses
CC   a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC   or C-terminal linker peptide which serves as the attachment point to a
CC   virus like particle or bacterial protein (the scaffold protein)
XX
SQ   Sequence 115 AA;

Qy   Query Match   58.4%; Score 356; DB 5; Length 115;
     Best Local Similarity   62.5%; Pred. No. 4.7e-34;
     Matches   70; Conservative   16; Mismatches   26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKSVPQGIDTLKNQTAHGE 63
              : |::|||||||:|||||||| : :||||||||||||:||||| ||||||||||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKRNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              :||:|||:||||||:::|:: ||| ||| ||:||||||||:|||:||||:|| ||
Db   64 TVBRLFKNLSLIKKYIDGQKKKCGBERRRVNQFLDYLQBFLGVWNTEWIIES 115

RESULT 14
AAO30453
ID   AAO30453 standard; protein; 115 AA.
XX
AC   AAO30453;
XX
DT   22-SEP-2003 (first entry)
XX
DE   Human mature interleukin 5 (IL5) protein.
XX
KW   Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW   tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
KW   IL5; human.
XX
OS   Homo sapiens.
XX
PN   WO2003042244-A2.
XX
PD   22-MAY-2003.
XX
PF   15-NOV-2002; 2002WO-DK000764.
XX
PR   16-NOV-2001; 2001DK-00001702.
PR   16-NOV-2001; 2001US-0331575P.
XX
PI   Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX
PA   (PHAR-) PHARMEXA AS.
PA   (KLYS/) KLYSNER S.
PA   (NIEL/) NIELSEN F S.
PA   (BRAT/) BRATT T.
PA   (VOLD/) VOLDBORG B.
PA   (MOUR/) MOURITSEN S.
XX
PT   New immunogenic analogue of a polymeric protein, useful for preparing a
PT   composition for treating inflammatory diseases e.g. arthritis.
XX
PS   Disclosure; Page 105; 196pp; English.
XX
CC   The invention relates to immunogenic analogues of multimeric proteins
CC   such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC   factor alpha (TNF, TNFalpha) and methods for production of immunogenic

CC   analogues. The immunogenic analogue is useful for preparing a composition
CC   for treating inflammatory diseases, e.g., arthritis. It is also used in
CC   gene therapy. The present sequence is human mature IL5 protein. This
CC   sequence is used to illustrate the method of the invention
XX
SQ   Sequence 115 AA;

Qy   Query Match   58.4%; Score 356; DB 6; Length 115;
     Best Local Similarity   62.5%; Pred. No. 4.7e-34;
     Matches   70; Conservative   16; Mismatches   26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKSVPQGIDTLKNQTAHGE 63
              : |::|||||||:|||||||| : :||||||||||||:||||| ||||||||||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKRNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              :||:|||:||||||:::|:: ||| ||| ||:||||||||:|||:||||:|| ||
Db   64 TVBRLFKNLSLIKKYIDGQKKKCGBERRRVNQFLDYLQBFLGVWNTEWIIES 115

RESULT 15
ADKI7208
ID   ADKI7208 standard; protein; 115 AA.
XX
AC   ADKI7208;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Human interleukin-5 processed for repetitive antigen array.
XX
KW   antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
KW   interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
KW   allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
XX
OS   Homo sapiens.
XX
PN   WO2003040164-A2.
XX
PD   15-MAY-2003.
XX
PF   07-NOV-2002; 2002WO-EP012455.
XX
PR   07-NOV-2001; 2001US-0331045P.
PR   18-JAN-2002; 2002US-0050902.
PR   21-JAN-2002; 2002WO-IB000166.
PR   19-JUL-2002; 2002US-0396636P.
XX
PI   Bachmann M, Jennings G, Sonderegger I;
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PT   Composition comprising an ordered and repetitive antigen or antigenic
PT   determinant array, useful as a medicament, or for manufacturing a
PT   medicament for treating allergic eosinophilic diseases, e.g. asthma, or
PT   Hodgkin's lymphoma.
XX
PS   Disclosure; SEQ ID NO 234; 245pp; English.
XX
CC   The invention relates to a composition comprising a virus-like particle
CC   and at least one antigen, which is a protein or peptide of interleukin
CC   (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
CC   core particle with at least one first attachment site and at least one
CC   antigen with at least one second attachment site, where the antigen is a
CC   protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
CC   is an attachment site naturally occurring with the
CC   antigen or antigenic determinant. The second attachment site is capable
CC   of association to the first attachment site, and where the antigen or
CC   antigenic determinant and the core particle interact through the
CC   association to form an ordered and repetitive antigen array. The
CC   compositions are useful as medicaments, or for manufacturing a medicament
CC   or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or

CC   Hodgkin's lymphoma and related diseases. This sequence is used to
CC   generate the compound of the invention.
XX
SQ   Sequence 115 AA;

Query Match   58.4%; Score 356; DB 7; Length 115;
Best Local Similarity   62.5%; Pred. No. 4.7e-34;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVPQGIDTLKNQTPAHGE 63
            | |:.|| ||||||||| |.|:.|:|||.| :.|:||||| :.||||||.|:||::.
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
            |:.:|||||||||||::|: ||||| ||||||||||:|||||||||||
Db   64 TVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWIIES 115

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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: August 4, 2005, 17:01:52 ; Search time 29.0964 Seconds
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                                             295.042 Million cell updates/sec

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Perfect score: 610
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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

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Issued Patents AA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	610	100.0	115	4	US-09-322-409-86	Sequence 86, Appl
2	610	100.0	115	4	US-09-451-527-86	Sequence 86, Appl
3	610	100.0	134	4	US-09-322-409-81	Sequence 81, Appl
4	610	100.0	134	4	US-09-451-527-81	Sequence 81, Appl
5	601	98.5	134	4	US-09-371-615A-2	Sequence 2, Appli
6	356	58.4	115	4	US-09-556-818-1	Sequence 1, Appli
7	356	58.4	134	1	US-08-284-393B-13	Sequence 13, Appli
8	356	58.4	134	4	US-08-759-628-9	Sequence 9, Appli
9	356	58.4	134	4	US-09-371-615A-7	Sequence 7, Appli
10	356	58.4	134	4	US-09-462-941-12	Sequence 12, Appli
11	356	58.4	134	5	PCT-US95-08950-13	Sequence 13, Appl
12	356	58.4	134	6	5324640-2	Patent No. 5324640
13	356	58.4	134	6	5324640-2	Patent No. 5324640
14	351	57.5	121	4	US-09-180-864-2	Sequence 2, Appli
15	347	56.9	133	4	US-09-371-615A-8	Sequence 8, Appli
16	339	55.6	126	4	US-09-556-818-6	Sequence 6, Appli
17	335	54.9	132	4	US-09-451-527-81	Sequence 81, Appl
18	332.5	54.5	126	4	US-09-556-818-28	Sequence 28, Appl
19	332.5	54.3	132	4	US-09-556-818-40	Sequence 40, Appl
20	331.5	54.2	132	4	US-09-556-818-4	Sequence 4, Appli
21	330.5	54.1	124	4	US-09-556-818-34	Sequence 34, Appl
22	330.5	54.1	124	4	US-09-556-818-9	Sequence 9, Appli
23	329.5	54.0	132	4	US-09-556-818-7	Sequence 7, Appli
24	328.5	53.9	130	4	US-09-556-818-32	Sequence 32, Appl
25	328.5	53.9	130	4	US-09-556-818-44	Sequence 44, Appl
26	324	53.1	147	4	US-09-556-818-44	Sequence 44, Appl
27	322.5	52.9	130	4	US-09-556-818-42	Sequence 42, Appl
28	321.5	52.7	124	4	US-09-556-818-5	Sequence 5, Appli
29	321.5	52.7	124	4	US-09-556-818-38	Sequence 38, Appli
30	321	52.6	124	4	US-09-556-818-17	Sequence 17, Appli
31	319.5	52.4	124	4	US-09-556-818-46	Sequence 46, Appl
32	318.5	52.2	130	4	US-09-556-818-56	Sequence 56, Appl
33	317	52.0	113	4	US-09-556-818-12	Sequence 12, Appl
34	317	52.0	130	4	US-09-556-818-21	Sequence 21, Appl
35	315.5	51.7	128	4	US-09-556-818-50	Sequence 50, Appl
36	311	51.0	145	4	US-09-556-818-60	Sequence 60, Appl
37	309.5	50.7	128	4	US-09-556-818-54	Sequence 54, Appl
38	308.5	50.6	128	4	US-09-556-818-8	Sequence 8, Appli
39	301.5	49.4	118	4	US-09-556-818-13	Sequence 13, Appl
40	301.5	49.4	122	4	US-09-556-818-18	Sequence 18, Appl
41	300.5	49.3	124	4	US-09-556-818-11	Sequence 11, Appl
42	300.5	49.1	124	4	US-09-556-818-52	Sequence 52, Appl
43	299.5	49.1	124	4	US-09-556-818-30	Sequence 30, Appl
44	293.5	48.1	122	4	US-09-556-818-36	Sequence 36, Appl
45	291.5	47.8	122	4	US-09-556-818-15	Sequence 15, Appl
46	290.5	47.6	130	4	US-09-556-818-18	Sequence 18, Appl
47	289.5	47.5	116	4	US-09-556-818-52	Sequence 52, Appl
48	289.5	47.5	128	4	US-09-556-818-20	Sequence 20, Appl
49	287.5	47.1	122	4	US-09-556-818-48	Sequence 48, Appl
50	282.5	46.3	122	4	US-09-556-818-16	Sequence 16, Appl
51	282.5	46.3	139	4	US-09-556-818-22	Sequence 22, Appl
52	282.5	46.3	116	4	US-09-556-818-14	Sequence 14, Appl
53	263.5	43.2	122	4	US-09-556-818-19	Sequence 19, Appl
54	261.5	42.9	686	4	US-09-914-259-33	Sequence 33, Appl
55	261.5	42.9	15	5	PCT-US94-06655-4	Sequence 4, Appl
56	72	11.8	683	4	US-09-270-767-46792	Sequence 46792, A
57	71	11.7	323	4	US-09-134-000C-5535	Sequence 5535, Ap
58	71	11.6	976	3	US-08-560-005-2	Sequence 2, Appli
59	69.5	11.4	976	3	US-09-195-868-14	Sequence 14, Appl
60	69.5	11.4	976	3	US-09-418-540-2	Sequence 2, Appli
61	69.5	11.4	976	3	US-09-969-528-2	Sequence 2, Appli
62	69.5	11.4	1187	3	US-08-664-962B-8	Sequence 8, Appli
63	69.5	11.4	1187	3	US-09-311-743-8	Sequence 8, Appli
64	69.5	11.4	1187	3	US-09-195-868-15	Sequence 15, Appl
65	69.5	11.4	1189	3	US-09-195-868-28	Sequence 28, Appl
66	68.5	11.2	517	4	US-09-248-796A-14631	Sequence 14631, A
67	68	11.1	406	1	US-09-902-540-13016	Sequence 13016, A
68	67.5	11.1	968	1	US-08-434-720-14	Sequence 14, Appl
69	67.5	11.1	1185	3	US-08-664-962B-2	Sequence 2, Appli
70	67.5	11.1	1185	3	US-09-311-743-2	Sequence 2, Appli
71	67	11.0	2311	3	US-09-311-743-9	Sequence 9, Appli
72	67	11.0	2311	3	US-08-934-386-9	Sequence 9, Appli
73	66.5	10.9	312	4	US-09-107-532A-6369	Sequence 6369, Ap
74	66	10.9	589	4	US-09-543-081A-4194	Sequence 4194, Ap
75	66	10.8	257	4	US-08-560-005-2	Sequence 2, Appli
76	66	10.8	604	4	US-09-248-796A-14638	Sequence 14638, A
77	66	10.8	2325	3	US-09-902-540-10284	Sequence 10284, A
78	66	10.8	2325	3	US-08-930-285-6	Sequence 6, Appli
79	66	10.8	2325	3	US-08-697-826A-10	Sequence 10, Appl
80	66	10.8	2325	3	US-09-367-293-5	Sequence 5, Appli
81	66	10.8	248	4	US-09-851-873-41	Sequence 41, Appl
82	65	10.7	177	4	US-09-328-352-6714	Sequence 6714, Ap
83	65	10.7	300	4	US-09-538-092-575	Sequence 575, App
84	65	10.7	738	4	US-09-270-767-42870	Sequence 42870, A
85	65	10.7	841	4	US-09-583-110-2805	Sequence 2805, Ap
86	65	10.6	205	4	US-09-107-532A-6672	Sequence 6672, Ap
87	65	10.6	186	4	US-09-252-991A-18473	Sequence 18473, A
88	65	10.6	205	4	US-09-107-433-3118	Sequence 3118, Ap
89	64.5	10.6	414	4	US-10-067-443-19	Sequence 19, Appl
90	64.5	10.6	414	4	US-10-067-443-2	Sequence 2, Appli
91	64.5	10.6	439	4	US-09-969-528-6	Sequence 6, Appli
92	64.5	10.6	489	4	US-08-695-551-6	Sequence 6, Appli
93	64	10.6	984	4	US-08-417-089-6	Sequence 6, Appli
94	64	10.5	260	4	US-09-328-352-6926	Sequence 6926, Ap
95	64	10.5	116	4	US-09-248-796A-19030	Sequence 19030, A
96	63.5	10.5	116	4	US-09-540-236-5350	Sequence 5350, Ap
97	63.5	10.4	448	4	US-09-513-999C-4105	Sequence 4105, Ap
98	63.5	10.4	448	2	US-09-540-236-3710	Sequence 3710, Ap
99	63.5	10.4	116	4	US-08-878-789-2	Sequence 2, Appli
100	63.5	10.4	508	4	US-09-272-789-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-322-409-86
; Sequence 86, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-86

Query Match   100.0%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.4e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
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RESULT 2
US-09-451-527-86
; Sequence 86, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-86

Query Match   100.0%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.4e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
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RESULT 3
US-09-322-409-81
; Sequence 81, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-81

Query Match   100.0%; Score 610; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 6.8e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
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RESULT 4
US-09-451-527-81
; Sequence 81, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-81

Query Match   100.0%; Score 610; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 6.8e-71;

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Db   20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy   61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
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Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   20 FAVENPMNRLIVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy   61 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
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RESULT 5
US-09-371-615A-2
Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 0360400170OUS00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-371-615A-2

Query Match   98.5%; Score 601; DB 4; Length 134;
Best Local Similarity 99.1%; Pred. No. 9.9e-70;
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 FAVENPMNRLIVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 FAVENPMNRLIVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy   61 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
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Db   80 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134
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RESULT 6
US-09-556-818-1
Sequence 1, Application US/09556818
; Patent No. 6746669
; GENERAL INFORMATION:
; APPLICANT: Klysner, Steen
; TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
; FILE REFERENCE: 0455-0428P
; CURRENT APPLICATION NUMBER: US/09/556,818
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (44)
; OTHER INFORMATION: Interchain disulphide bond to Cys-86 in SEQ ID
; OTHER INFORMATION: NO:1
; NAME/KEY: DISULFID
; LOCATION: (86)
; OTHER INFORMATION: Interchain disulphide bond to Cys-44 in SEQ ID
; OTHER INFORMATION: NO:1
US-09-556-818-1

Query Match   58.4%; Score 356; DB 4; Length 115;
Best Local Similarity 62.5%; Pred. No. 4e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

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Db    4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIPQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
        |:||||||||||||||||:|||||:||||||:||| ::||||||||| |
Db   64 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQEFLGVMNTEWIIES 115
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RESULT 7
US-08-284-393B-13
Sequence 13, Application US/0824393B
; GENERAL INFORMATION:
; Patent No. 5696234
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-13

Query Match   58.4%; Score 356; DB 1; Length 134;
Best Local Similarity 62.5%; Pred. No. 5e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

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Db   23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIPQGTLESQTVQGG 82

Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
        |:||||||||||||:|||:|||||:||||||:||| ::||||||||| |
Db   83 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQEFLGVMNTEWIIES 134
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RESULT 8
US-08-759-628-9
Sequence 9, Application US/08759628
; Patent No. 6225446
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.

```
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
    ADDRESSEE: DNAX Research Institute
    STREET: 901 California Avenue
    CITY: Palo Alto
    STATE: California
    COUNTRY: USA
    ZIP: 94304-1104
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC Compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/759,628
    FILING DATE: 05-DEC-1996
    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 60/008,574
    FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
    NAME: Ching, Edwin P.
    REGISTRATION NUMBER: 34,090
    REFERENCE/DOCKET NUMBER: DX0552Q
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-852-9196
    TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 9:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 134 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    FEATURE:
    NAME/KEY: Peptide
    LOCATION: 20..134
    OTHER INFORMATION: /note= "Peptide of Figure 1"
US-08-759-628-9
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Query Match            58.4%;    Score 356;  DB 3;  Length 134;
Best Local Similarity  62.5%;    Pred. No. 5e-38;
Matches 70;  Conservative 16;  Mismatches 26;  Indels 0;  Gaps 0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         | :|| |||||||:||| |||||||| ||:|:| :|:|| |||:|:|||::||  |||
Db  23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 82

Qy  64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
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Db  83 TVERLFKNLSLIKKYIDGQKKCCGBERRRVNQFLDYLQEFLGVMNTEWIIES 134
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RESULT 9
US-09-371-615A-7
Sequence 7, Application US/09371615A
Patent No. 6537781
GENERAL INFORMATION:
    APPLICANT: IDEXX LABORATORIES
    TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
        CANINE INTERLEUKIN 5
    FILE REFERENCE: 03604001700US00
    CURRENT APPLICATION NUMBER: US/09/371,615A
    CURRENT FILING DATE: 1999-08-10
    NUMBER OF SEQ ID NOS: 8
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 7
    LENGTH: 134
    TYPE: PRT
    ORGANISM: Homo sapiens
    FEATURE:
    OTHER INFORMATION: Interleukin 5
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US-09-371-615A-7

Query Match            58.4%;    Score 356;  DB 4;  Length 134;
Best Local Similarity  62.5%;    Pred. No. 5e-38;
Matches 70;  Conservative 16;  Mismatches 26;  Indels 0;  Gaps 0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         | :|| |||||||:||| |||||||| ||:|:| :|:|| |||:|:|||::||  |||
Db  23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 82

Qy  64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         :|:||||||||:|:|:||||||||||||||||||||||||||||||||||||
Db  83 TVERLFKNLSLIKKYIDGQKKCCGBERRRVNQFLDYLQEFLGVMNTEWIIES 134
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RESULT 10
US-09-462-941-12
Sequence 12, Application US/09462941
Patent No. 6608183
GENERAL INFORMATION:
    APPLICANT: Cox III, George N
    APPLICANT: Bolder Biotechnology, Inc.
    TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
    FILE REFERENCE: 4152-1-PUS
    CURRENT APPLICATION NUMBER: US/09/462,941
    CURRENT FILING DATE: 2000-01-14
    PRIOR APPLICATION NUMBER: 60/052,516
    PRIOR FILING DATE: 1997-07-14
    NUMBER OF SEQ ID NOS: 41
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 12
    LENGTH: 134
    TYPE: PRT
    ORGANISM: Homo sapiens
US-09-462-941-12
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Query Match            58.4%;    Score 356;  DB 4;  Length 134;
Best Local Similarity  62.5%;    Pred. No. 5e-38;
Matches 70;  Conservative 16;  Mismatches 26;  Indels 0;  Gaps 0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         | :|| |||||||:||| |||||||| ||:|:| :|:|| |||:|:|||::||  |||
Db  23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 82

Qy  64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         :|:||||||||:|:|:||||||||||||||||||||||||||||||||||||
Db  83 TVERLFKNLSLIKKYIDGQKKCCGBERRRVNQFLDYLQEFLGVMNTEWIIES 134
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RESULT 11
PCT-US95-08950-13
Sequence 13, Application PCT/US9508950
GENERAL INFORMATION:
    APPLICANT: Zurawski, Sandra M.
    APPLICANT: Zurawski, Gerard
    TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
    NUMBER OF SEQUENCES: 13
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: DNAX Research Institute
    STREET: 901 California Avenue
    CITY: Palo Alto
    STATE: California
    COUNTRY: USA
    ZIP: 94304-1104
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC Compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US95/08950
    FILING DATE:
    CLASSIFICATION:
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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/284,393
  FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Ching, Edwin P.
  REGISTRATION NUMBER: 34,090
  REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-852-9196
  TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 13:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 134 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: protein
PCT-US95-08950-13
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RESULT 12
5324640-2
;Patent No. 5324640
APPLICANT: Honjo, Tasuku;Takatsu, Kiyoshi;Severinson, Eva
TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
;PROCESS OF PRODUCING SAID FACTOR
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/99,467
;SEQ ID NO:2:
  FILING DATE: 21-SEP-1987
LENGTH: 134.

Query Match        58.4%;  Score 356;  DB 5;  Length 134;
Best Local Similarity  62.5%;  Pred. No. 5e-38;
Matches  70;  Conservative 16;  Mismatches 26;  Indels 0;  Gaps 0;

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RESULT 13
5324640-2
;Patent No. 5324640
APPLICANT: Honjo, Tasuku;Takatsu, Kiyoshi;Severinson, Eva
TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
;PROCESS OF PRODUCING SAID FACTOR
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/99,467
  FILING DATE: 21-SEP-1987
;SEQ ID NO:2:
LENGTH: 134

Query Match        58.4%;  Score 356;  DB 6;  Length 134;
Best Local Similarity  62.5%;  Pred. No. 5e-38;
Matches  70;  Conservative 16;  Mismatches 26;  Indels 0;  Gaps 0;

Qy    4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
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RESULT 14
US-09-180-864-2
;Sequence 2, Application US/09180864
Patent No. 6465616
GENERAL INFORMATION:
  APPLICANT: Lopez, Angel
  APPLICANT: Vadas, Matthew
  APPLICANT: Shannon, Frances
  APPLICANT: Bastiras, Stan
  APPLICANT: Hey, Allan W
  TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
  FILE REFERENCE: 9972Z
  CURRENT APPLICATION NUMBER: US/09/180,864
  CURRENT FILING DATE: 1999-04-12
  PRIOR APPLICATION NUMBER: 08/591,438
  PRIOR FILING DATE: 1994-07-28
  NUMBER OF SEQ ID NOS: 8
  SOFTWARE: PatentIn Ver. 2.1
;SEQ ID NO 2
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  TYPE: PRT
  ORGANISM: modified IL-5
US-09-180-864-2

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Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
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RESULT 15
US-09-371-615A-8
;Sequence 8, Application US/09371615A
Patent No. 6537781
GENERAL INFORMATION:
  APPLICANT: IDEXX LABORATORIES
  TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
;TITLE OF INVENTION: CANINE INTERLEUKIN 5
  FILE REFERENCE: 036040017OOUS00
  CURRENT APPLICATION NUMBER: US/09/371,615A
  CURRENT FILING DATE: 1999-08-10
  NUMBER OF SEQ ID NOS: 8
  SOFTWARE: FastSEQ for Windows Version 3.0
  SEQ ID NO 8
  LENGTH: 133
  TYPE: PRT
  ORGANISM: Mus musculus
  FEATURE:
  OTHER INFORMATION: Interleukin 5
US-09-371-615A-8

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Best Local Similarity  58.4%;  Pred. No. 7.3e-37;
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Matches 66; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on:　　　　　August 4, 2005, 17:11:16 ; Search time 97.9116 Seconds
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Title:　　　　　　US-10-787-382-10
Perfect score:　610
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Scoring table:　BLOSUM62
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Maximum DB seq length: 200000000
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	610	100.0	115	14	US-10-218-654-86	Sequence 86, Appl
3	610	100.0	115	14	US-10-262-439-86	Sequence 86, Appl
4	610	100.0	115	16	US-10-787-382-10	Sequence 10, Appl
5	610	100.0	134	9	US-09-755-633-5	Sequence 5, Appli
6	610	100.0	134	14	US-10-218-654-81	Sequence 81, Appl
7	610	100.0	134	14	US-10-262-439-81	Sequence 81, Appl
8	610	100.0	134	16	US-10-787-382-5	Sequence 5, Appli
9	610	100.0	115	16	US-10-658-834A-588	Sequence 588, App
10	357	58.5	115	16	US-10-658-834A-569	Sequence 569, App
11	357	58.5	287	14	US-10-295-074-13	Sequence 13, Appl

12	357	58.5	287	16	US-10-846-911-13	Sequence 13, Appl
13	357	58.4	115	16	US-10-289-454-234	Sequence 234, App
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15	357	58.4	115	16	US-10-050-898-234	Sequence 234, App
16	356	58.4	115	14	US-10-289-454-233	Sequence 233, App
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18	356	58.4	115	14	US-10-289-454-233	Sequence 233, App
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21	356	58.4	123	14	US-10-050-902-233	Sequence 233, App
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99	74	12.1	15	9	US-09-755-633-20	Sequence 20, Appl
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ALIGNMENTS

; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-86

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RESULT 1
US-09-755-633-10
; Sequence 10, Application US/09755633
; Patent No. US2002012720A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
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; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-10

Query Match   100.0%;   Score 610;   DB 9;   Length 115;
Best Local Similarity   100.0%;   Pred. No. 1.2e-63;
Matches 115;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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RESULT 2
US-10-218-654-86
; Sequence 86, Application US/10218654
; Publication No. US20030096009A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13

RESULT 3
US-10-262-439-86
; Sequence 86, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
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; SEQ ID NO 86
; LENGTH: 115
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; ORGANISM: Canis familiaris
US-10-262-439-86

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RESULT 4
US-10-787-382-10
; Sequence 10, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-787-382-10

Query Match   100.0%; Score 610; DB 16; Length 115;
Best Local Similarity   100.0%; Pred. No. 1.2e-63;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
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Db   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60

Qy   61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

RESULT 5
US-09-755-633-5
; Sequence 5, Application US/0975563
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-5

Query Match   100.0%; Score 610; DB 9; Length 134;
Best Local Similarity   100.0%; Pred. No. 1.4e-63;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy   61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134

RESULT 6
US-10-218-654-81

; Sequence 81, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-81

Query Match   100.0%; Score 610; DB 14; Length 134;
Best Local Similarity   100.0%; Pred. No. 1.4e-63;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy   61 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134

RESULT 7
US-10-262-439-81
; Sequence 81, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-81

Query Match   100.0%; Score 610; DB 14; Length 134;
Best Local Similarity   100.0%; Pred. No. 1.4e-63;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 FAVENPMNRLVAEFLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

RESULT 8
US-10-787-382-5
; Sequence 5, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-787-382-5

Query Match   100.0%;   Score 610; DB 16;   Length 134;
Best Local Similarity   100.0%;   Pred. No. 1.4e-63;
Matches 115; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 79

Qy   61 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 HGEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134

RESULT 9
US-10-658-834A-588
; Sequence 588, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 588
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-588

Query Match   58.7%;   Score 358; DB 16;   Length 115;

RESULT 10
US-10-658-834A-569
; Sequence 569, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 569
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-569

Query Match   58.5%;   Score 357; DB 16;   Length 115;
Best Local Similarity   62.5%;   Pred. No. 7.8e-34;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              ||:||||||||||||||||||||:||||:||:|:|:||||||||||||||||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLQIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

RESULT 11
US-10-295-074-13
; Sequence 13, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P10133DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 13
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human IL5 monomers joined by diglycine linker and including t
; OTHER INFORMATION: erminally positioned P30 and P2 epitopes
US-10-295-074-13

Best Local Similarity   62.5%;   Pred. No. 6e-34;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
              :|||||||||:||||:|:|:||||:|:|||||||:||||||||||||||||:|:|||||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              ||:||||||||||||||||||||:||||:||:|:|:||||||||||||||||
Db   4 TVERLFKNLSLIKKYIDGQKKKCGNERRRVNQFLDYLQEFLGVMNTEWIIES 115

RESULT 12
US-10-846-911-13
; Sequence 13, Application US10846911
; Publication No. US20040258660A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen
; APPLICANT: NIELSEN, Finn Stausholm
; APPLICANT: BRATT, Tomas
; APPLICANT: VOLDBORG, Bjorn
; APPLICANT: MOURITSEN, Soren
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: 67454-2018
; CURRENT APPLICATION NUMBER: US/10/846,911
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK02/00764
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,575
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: PA 2001 01702
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human IL5 monomers joined by diglycine linker and including
; OTHER INFORMATION: terminally positioned P30 and P2 eptopes
US-10-846-911-13

Query Match   58.5%;   Score 357; DB 14; Length 287;
Best Local Similarity   61.9%;   Pred. No. 2.6e-33;
Matches   70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy   3 VENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHG 62
            :|:|||||||||||:|||||||||||::||||||:||:|||||||||::||||::|
Db   43 LEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQG 102

Qy   63 EAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
            |:|:|||:||:|||:|:|: |||| ||||:||:||||||:||||:|||| ||
Db 103 GTVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQBFLGVWNNTEWIIES 155

RESULT 13
US-10-289-454-234
; Sequence 234, Application US20030157479A1
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 234
; LENGTH: 115
; TYPE: PRT
; ORGANISM: processed human IL-5
US-10-289-454-234

Query Match   58.4%;   Score 357; DB 16; Length 287;
Best Local Similarity   61.9%;   Pred. No. 2.6e-33;
Matches   70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy   3 VENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHG 62
            :|:|||||||||||:|||||||||||::||||||:||:|||||||||::||||::|
Db   43 LEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQG 102

Qy   63 EAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
            |:|:|||:||:|||:|:|: |||| ||||:||:||||||:||||:|||| ||
Db 103 GTVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQBFLGVWNNTEWIIES 155

Query Match   62.5%;   Score 356; DB 14; Length 115;
Best Local Similarity   62.5%;   Pred. No. 1e-33;
Matches   70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
            |:|||||||||||:|||||||||||::||||||:||:|||||||||::||||::|||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
            |:|:|||:||:|||:|:|: |||| ||||:||:||||||:||||:|||| ||
Db   64 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQBFLGVWNNTEWIIES 115

RESULT 14
US-10-050-902-234
; Sequence 234, Application US10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 234
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-234

Query Match   58.4%;   Score 356; DB 14; Length 115;
Best Local Similarity   62.5%;   Pred. No. 1e-33;
Matches   70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
            |:|||||||||||:|||||||||||::||||||:||:|||||||||::||||::|||
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
            |:|:|||:||:|||:|:|: |||| ||||:||:||||||:||||:|||| ||
Db   64 TVERLFKNLSLIKKYIDGQKKKCGEBRRRVNQFLDYLQBFLGVWNNTEWIIES 115

RESULT 15
US-10-050-898-234
; Sequence 234, Application US10050898

; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 234
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-234

Query Match   58.4%;   Score 356; DB 14;   Length 115;
Best Local Similarity   62.5%;   Pred. No. 1e-33;
Matches 70; Conservative 16; Mismatches 26; Indels   0; Gaps   0;

Qy   4 ENPMNRLVARTLTLLSTRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
              | |||||| |:||| :| | | |||||| || ||||||| |||:| |||||| ||||:
Db   4 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 63

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              : | ||||||||| :| || |:|| :: |:|||||||| |||||||||||||
Db   64 TVERLFQNLSLIKKYIDGQKKKCGEERRRVVNQFLDYLQEFLGVWNTEWIES 115

Search completed: August 4, 2005, 17:30:12
Job time : 98.9916 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: August 4, 2005, 16:59:07 ; Search time 22.6305 Seconds
(without alignments)
488.938 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVARTLTLLST...........FLDYLQVFLGVINTEWTPES 115

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Database :   PIR_79:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	491	80.5	134	2	JC5116	interleukin-5 prec
2	356	58.4	134	1	A28477	interleukin-5 prec
3	347	56.9	133	1	ICMS5	interleukin-5
4	332	54.4	132	1	A48418	interleukin-5 prec
5	258	78.5	132	2	T47758	hypothetical prote
6	74.5	12.9	1232	2	B39432	ATP-dependent deox
7	73.5	12.2	1232	2	T47757	hypothetical prote
8	73	12.0	253	2	B39432	hypothetical prote
9	73	12.0	1199	2	G69698	RNA polymerase (be
10	72.5	11.9	451	2	S33816	hypothetical prote
11	72.5	11.9	649	2	S33813	kinesin light chai
12	72.5	11.9	677	2	S33814	kinesin light chai
13	72	11.8	686	2	S33815	kinesin light chai
14	72	11.8	401	2	S28653	kinesin light chai
15	71	11.6	216	2	B69498	hypothetical prote
16	71	11.6	300	2	F84594	hypothetical prote
17	71	11.6	328	2	F64187	hypothetical prote
18	71	11.6	446	2	T38698	hypothetical prote
19	70	11.5	461	2	T38698	hypothetical prote
20	69.5	11.5	933	2	A59250	myosin - Acetabula
21	69.5	11.4	253	2	C97331	arac-type DNA-bind
22	69.5	11.4	331	2	G83876	p-aminobenzoate sy
23	69.5	11.4	1188	2	JC4889	hypothetical prote
24	69	11.3	215	2	F45355	hypothetical prote
25	69	11.3	346	2	S66958	phosphatidylinosit
26	69	11.3	759	2	F64662	ORF2 protein - Aut
27	69	11.3	1871	2	D96698	UFB1 protein - yea
28	68.5	11.2	1894	2	T02155	trans-Golgi membra
29	68.5	11.2	190	2	S23712	probable DNA polym
						DNA-directed DNA p
						interferon alpha-I
						hypothetical prote
30	68.5	11.2	709	2	T32089	hypothetical prote
31	68.5	11.2	1102	2	S65235	probable membrane
32	68	11.1	215	2	B72854	AcOrf-34 protein -
33	68	11.1	414	2	G84311	probable
34	68	11.1	529	2	S35306	hypothetical prote
35	68	11.1	570	2	CO2PCD	phytoene dehydroge
36	68	11.1	1055	2	T10432	cdc10 start contro
37	67.5	11.0	767	2	T28748	DNA-directed RNA p
38	68	11.1	1621	2	A82255	hypothetical prote
39	67.5	11.0	1189	2	JC6118	SH2-containing ino
40	67	11.0	356	2	S15156	AcMNPV orf34 - Bom
41	67	11.0	570	2	AG1228	myosin heavy chain
42	67	10.9	2311	2	T06161	DNA polymerase bet
43	66.5	10.9	274	2	T21284	acetyl-CoA carboxy
44	66.5	10.9	590	2	H71977	hypothetical prote
45	66.5	10.8	119	2	T37844	hypothetical prote
46	66	10.8	463	2	G87441	SCF complex protei
47	66	10.8	2325	2	T28748	DNA-directed RNA p
48	66	10.8	248	2	T22235	hypothetical prote
49	66	10.8	368	2	T02921	acetyl-CoA carboxy
50	65.5	10.7	520	2	A46652	acetyl-CoA carboxy
51	65.5	10.7	2269	2	A69774	probable acyl-CoA
52	65.5	10.7	295	2	T28677	hypothetical prote
53	65.5	10.7	377	2	E71416	glucosamine-6-phos
54	65	10.7	664	2	A69636	integrase homolog
55	65	10.7	738	1	AE1991	hypothetical prote
56	65	10.7	886	2	JX0336	rhoptry protein -
57	65	10.7	248	2	S51380	hypothetical prote
58	65	10.7	453	2	AD0831	glycine-tRNA ligas
59	65	10.7	886	2	A46652	hypothetical prote
60	65	10.7	1460	2	T00095	succinate dehydrog
61	64.5	10.6	1685	2	JC6180	protein kinase STE
62	64.5	10.6	189	1	AC2012	transcription regu
63	64.5	10.6	220	2	F89936	stearoyl-CoA 9-des
64	64.5	10.6	225	2	S50006	hypothetical prote
65	64.5	10.6	246	2	E83517	conserved hypothet
66	64.5	10.6	451	1	B95085	preprotein translo
67	64	10.6	366	2	E83517	conserved hypothet
68	64	10.5	437	2	AI1581	DNA polymerase bet
69	64	10.5	453	2	D81302	probable ATP/GTP-b
70	64	10.5	570	2	NBHUH	complement factor
71	64	10.5	588	2	H90192	hypothetical prote
72	64	10.5	1231	1	H81313	ATP-dependent DNA
73	63.5	10.4	380	2	T15728	hypothetical prote
74	63.5	10.4	691	2	B90389	conserved hypothet
75	63.5	10.4	693	2	G69634	virion tegument pr
76	63.5	10.4	1012	2	P90037	glutamate synthase
77	63.5	10.4	1520	2	D88637	protein W09G12.1	
78	63.5	10.3	133	2	D86686	hypothetical prote
79	63	10.3	281	2	D88637	hypothetical prote
80	63	10.3	290	2	T35529	anthranilate phosp
81	63	10.3	354	2	E86159	hypothetical prote
82	63	10.3	453	2	T32961	hypothetical prote
83	63	10.3	543	2	D82824	regulator of patho
84	63	10.3	569	2	T32221	hypothetical prote
85	63	10.3	670	2	A40636	ferric enterobacti
86	63	10.3	746	2	A96586	hypothetical prote
87	63	10.3	1250	2	SJHUA	spectrin alpha cha
88	62.5	10.2	269	1	C69651	proliopoprotein di
89	62.5	10.2	2429	1	C69651	virion tegument pr
90	62.5	10.2	544	2	T42932	probable regulator
91	62.5	10.2	269	2	A57376	alpha-toxin - Clos
92	62.5	10.2	746	2	S55805	variant-specific s
93	62.5	10.2	2178	2	S55805	polyketide synthet
94	62	10.2	2228	2	T14029	probable ATP/GTP-b
95	62	10.2	4930	2	E69679	hypothetical prote
96	62	10.2	187	2	A81291	conserved hypothet
97	62	10.2	257	2	B89775	conserved hypothet
98	62	10.2	297	2	AD0800	preprotein translo
99	62	10.2	305	2	C86745	preprotein translo
100	62	10.2	437	2	JC5115	interferon alpha-I
				553	2	G71543	probable fructose-

ALIGNMENTS

RESULT 1

JC5116
interleukin-5 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: JC5116
Gene 176, 273-274, 1996
R;Mertens, B.; Gobright, E.; Seow, H.F.
A;Reference number: JC5116
A;Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.
A;Accession: JC5116; MUID:9705944; PMID:8918267
A;Molecule type: mRNA
A;Residues: 1-134 <MER>
A;Cross-references: UNIPROT:P52173; EMBL:Z67872; NID:g1113120; PIDN:CAA91779.1; PID:g111
C;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
C;Experimental source: lymphocytes
C;Comment: This protein plays a role in the eosinophilia associated with parasitic disea
C;Genetics:
A;Gene: IL-5
A;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: interleukin-5 #status predicted <MAT>
F;63/Disulfide bonds: interchain (to 105) #status predicted
F;76,90/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;105/Disulfide bonds: interchain (to 63) #status predicted

Qy   2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTPAH 61
          |||||||||||||||||||||||||:|||||||||:||||||||||||||||||||||
Db   21 AVESTMNRLVAETLTLLSSHRTLLIGDGNLMIPTPQHTNHQLCIBEVFQGIDTLKNQTAQ 80

Qy   62 GEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFPLDYLQVFLGVINTEWTPES 115
          |||||||||||:||||:|:|||||||||||||:||||||||||||||||| ||
Db   81 GDAVKKIFQNLSLIKEYIDLQKRKCGGERWRVKQFLDYLQVFLGVINTEWTMES 134

Query Match   80.5%; Score 491.; DB 2; Length 134;
Best Local Similarity 81.6%; Pred. No. 8e-42;
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

RESULT 2

A28477
interleukin-5 precursor - human
N;Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A28477; A33883; A26112; A39881; JX0106; S15775
R;Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.
J. Biol. Chem. 262, 16580-16584 1987
A;Title: Molecular cloning and structure of the human interleukin-5 gene.
A;Reference number: A28477; MUID:88050042; PMID:2824500
A;Accession: A28477
A;Molecule type: DNA
A;Residues: 1-134 <TAN>
A;Cross-references: UNIPROT:P05113; GB:J03478; NID:g186338; PIDN:AAA74469.1; PID:g386822
R;Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Mayo, G.; Clutterbuck, E.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6629-6633, 1987
A;Title: Molecular cloning, nucleotide sequence, and expression of the gene encoding hum
A;Reference number: A33883; MUID:88016145; PMID:3498940
A;Accession: A33883
A;Molecule type: DNA
A;Residues: 1-134 <CAM>
A;Cross-references: GB:J02971; NID:g163040; PIDN:AAA98620.1; PID:g386823
R;Azuma, C.; Tanabe, T.; Konishi, M.; Kinashi, T.; Noma, T.; Tanabe, Y.; Ta
Nucleic Acids Res. 14, 9149-9158, 1986
A;Title: Cloning of cDNA for human T-cell replacing factor (interleukin-5) and compariso
A;Reference number: A26112; MUID:87066782; PMID:3024129
A;Accession: A26112
A;Molecule type: mRNA
A;Residues: 1-134 <AZU>
A;Cross-references: GB:X04688; NID:g33835; PIDN:CAA28390.1; PID:g33836

R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmell]
de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hume
A;Reference number: A39881; MUID:88041112; PMID:2823259
A;Accession: A39881
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-134 <YOK>
R;Proudfoot, A.E.I.; Davies, J.G.; Turcatti, G.; Wingfield, P.T.
FEBS Lett. 283, 61-64, 1991
A;Title: Human interleukin-5 expressed in Escherichia coli: assignment of the disulfide b
A;Reference number: S15775; MUID:91243878; PMID:2037074
A;Accession: A39881
A;Contents: annotation; disulfide bonds
R;Minamitake, Y.; Kodama, S.; Katayama, T.; Adachi, H.; Tanaka, S.; Tsujimoto, M.
J. Biochem. 107, 292-297, 1990
A;Title: Structure of recombinant human interleukin 5 produced by chinese hamster ovary c
A;Reference number: JX0106; MUID:90299868; PMID:2361960
A;Accession: A39881
A;Contents: annotation; disulfide bonds; glycosylation sites
C;Genetics:
A;Gene: GDB:IL5
A;Cross-references: GDB:120097; OMIM:147850
A;Map position: 5q31.1-5q31.1
C;Introns: 48/3; 59/3; 102/3
C;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: interleukin-5 #status predicted <MAT>
F;22/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;47,90/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;63/Disulfide bonds: interchain (to 105) #status experimental
F;105/Disulfide bonds: interchain (to 63) #status experimental

Query Match   58.4%; Score 356; DB 1; Length 134;
Best Local Similarity 62.5%; Pred. No. 2.3e-28;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

Qy   4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTPAHGE 63
          ||:||||||||||| |||||||||||||||:||||||||||||||||||||||||||||
Db   23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 82

Qy   64 AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFPLDYLQVFLGVINTEWTPES 115
          |:||:||||||||||||:||:|:|||||||||:|||||||||||||| ||||
Db   83 TVERLFKNLSLIKKYIDGQKKKCCGEERRVNQFLDYLQEFLGVMNTEWIIES 134

RESULT 3

ICM55
interleukin-5 precursor - mouse
N;Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil di
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00807; A38758; A24898; J50077; PH0102; B39881
R;Campbell, H.D.; Sanderson, C.J.; Wang, Y.; Hort, Y.; Martinson, M.E.; Tucker, W.Q.J.; S
Eur. J. Biochem. 174, 345-352, 1988
A;Title: Isolation, structure and expression of cDNA and genomic clones for murine eosino
n-5.
A;Reference number: S00807; MUID:88254802; PMID:3133208
A;Accession: S00807
A;Molecule type: DNA
A;Residues: 1-133 <CAM>
A;Cross-references: UNIPROT:P04401; EMBL:X06271; NID:g952685; PIDN:CAA29607.1; PID:g52686
A;Accession: A38758
A;Molecule type: mRNA
A;Residues: 1-133
A;Cross-references: EMBL:X06270; NID:g952687; PIDN:CAA29606.1; PID:g52688
R;Kinashi, T.; Harada, N.; Severinson, E.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma, C
Nature 324, 70-73, 1986
A;Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with
A;Reference number: A24898; MUID:87065032; PMID:3024009
A;Accession: A24898
A;Molecule type: mRNA
A;Residues: 1-133 <KIN>

Query Match   49.?%
Best Local Similarity
Matches ...

A;Cross-references: EMBL:X04601; NID:g54898; PIDN:CAA28266.1; PID:g54899
R;Mizuta, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.
Growth Factors 1, 51-57, 1988
A;Title: Molecular cloning and structure of the mouse interleukin-5 gene.
A;Reference number: JS0077; MUID:90180853; PMID:3078564
A;Accession: JS0077
A;Molecule type: DNA
A;Residues: 1-133 <MIZ>
R;Takahashi, T.; Yamaguchi, N.; Mita, S.; Yamaguchi, Y.; Suda, T.; Tominaga, A.; Kikuchi
Mol. Immunol. 27, 911-920, 1990
A;Title: Structural comparison of murine T-cell (B151K12)-derived T-cell-replacing facto
A;Reference number: PH0102; MUID:91015093; PMID:2215480
A;Accession: PH0102
A;Molecule type: protein
A;Residues: 21-45,'X',47 <TAK>
R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum
A;Reference number: A39881; MUID:88041112; PMID:2823259
A;Accession: B39881
A;Status: preliminary; not compared with conceptual translation

Query Match   56.9%; Score 347; DB 1; Length 133;
Best Local Similarity 58.4%; Pred. No. 1.8e-27;
Matches   66; Conservative   18; Mismatches   29; Indels   0; Gaps   0;

Qy   2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTPENKNHQLCIKEVFQGIDTLKNQTAH 61
          :||:|||.|:||||.||:|:|||.|:.:.||.||.|.||||||||.|.|||||.|||||.
Db   20 AMEIPMSTVVKETLIQLSAHRALITSNETMRLPVPFHKNHQLCIGIFQGIDLIKNQTVR 78

Qy   62 GEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPE 114
          |.:|::|||||||||::|:.||:.|.|||||:|::||||||:|||||.|||.||
Db   79 GGTVEMLFQNLSLIKKYIDGQKEKCGEERRKTRHFLDYLQEFLGVWSTEWAME 131

RESULT 4
A48418
interleukin-5 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Experimental source: cell line TR5-1
A;Accession: A48418; S37641
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Uberla, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstei
Cytokine 3, 72-81, 1991
A;Title: The rat interleukin-5 gene: characterization and expression by retroviral gene
A;Reference number: A48418; MUID:91355638; PMID:1653053
A;Accession: A48418
A;Molecule type: protein
A;Residues: 1-132 <UBE>
A;Cross-references: UNIPROT:Q08125; EMBL:X54419; NID:g313254; PIDN:CAA38283.1; PID:g3132
C;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-132/Product: interleukin-5 #status predicted <MAT>
F;45,74,88/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;61/Disulfide bonds: interchain (to 103) #status predicted
F;103/Disulfide bonds: interchain (to 61) #status predicted

Query Match   54.4%; Score 332; DB 1; Length 132;
Best Local Similarity 56.6%; Pred. No. 5.7e-26;
Matches   64; Conservative   18; Mismatches   31; Indels   0; Gaps   0;

Qy   2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTPENKNHQLCIKEVFQGIDTLKNQTAH 61
          :||:|||.|:||||.||:|:|||.|:.:.||.||.|.||||||||.|.|||||.|||||.
Db   20 AMEIPMSTVVKETLIQLSAHRALITSNETMRLPVPFHKNHQLCIGIFQGIDLIKNQTVR 78

Qy   62 GEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPE 114
          |.:|::|||||||||::|:.||:.|.|||||:|::||||||:|||||.|||.||
Db   79 GGTVEILFQNLSLIKKYIDRQKEKCGEERRTRQFLDYLQEFLGVWSTEWAME 132

RESULT 5
T47758
hypothetical protein F2413.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47758
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; N
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <NYA>
A;Cross-references: UNIPROT:Q9M1K0; EMBL:AL138655
C;Experimental source: cultivar Columbia; BAC clone F2413
C;Genetics:
A;Map position: 3
A;Introns: 109/3
A;Note: P2413.60
C;Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match   12.9%; Score 78.5; DB 2; Length 258;
Best Local Similarity 26.8%; Pred. No. 2.4;
Matches   22; Conservative   15; Mismatches   38; Indels   7; Gaps   2;

Qy   9 RLVAETLTLLSTHRTWLIGDGNLMIPPTPENKNHQLCIKEVFQGID----TLKNQTAHGEA 64
          .||:.:..:|:|.|:..:|||:.|.....:.|:...:...:..:|| |||:::..|.
Db 161 KAVANYISTVSATR---LGDNEVMVQISSSKIHNFSISNVLSGLEEDRFVLVDMSSSRSQ 217

Qy   65 VDKLFQNLSLIKEHIERQKKRRC 86
          ..:||.:|.|::..||||.|:.|
Db 218 GERLFYTLHLQVBKIENYKLNC 239

RESULT 6
B39432
ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis
N;Alternate names: ATP-dependent exonuclease synthesis protein AddA
C;Species: Bacillus subtilis
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
C;Accession: B39432; H69582
R;Kooistra, J.; Venema, G.
J. Bacteriol. 173, 3644-3655, 1991
A;Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-c
A;Reference number: A39432; MUID:91267926; PMID:1646786
A;Accession: B39432
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1232 <KOO>
A;Cross-references: UNIPROT:P23478; GB:M63489; NID:g142438; PIDN:AAA22201.1; PID:g142440
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bereng
A;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A;Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel,
Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
Koerter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: H69582
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Molecule type: DNA
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1232 <KUN>
A;Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12903.1; PID:e1183065;
A;Experimental source: strain 168
C;Genetics:
A;Gene: adda
A;Keywords: nucleotide binding; P-loop
P;30-37/Region: nucleotide-binding motif A (P-loop)

Query Match   12.2%; Score 74.5; DB 2; Length 1232;
Best Local Similarity   22.2%; Pred. No. 37;
Matches 24; Conservative 24; Mismatches 37; Indels 23; Gaps 4;

Qy   3 VENPMRLVAFTLTLLSTHRTWLIG--DGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTA 60
        :||| : :|:: |:| |||:: ||| :|: |::
Db 633 IDNPY----QDIPLASVLRSPIVGADENELSLIRLENKKAPY------YEAMKDYLA 679

Qy   61 HGRAVDKLFQNLSLIKEHIERQK--------KRCAGERWRVTKFLDYL 100
        |:|:|:| ||:|:|:|:|||::| | |: :|:::|:
Db 680 AGDRSDELYQKLINTFYGHLQKWRAFSKNHSVSELIWEVYRDTKYMDYV 727

RESULT 7
T47757
hypothetical protein F24I3.50 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
A;Accession: T47757
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <NYA>
A;Cross-references: UNIPROT:Q9MIK1; EMBL:AL138655
A;Experimental source: cultivar Columbia; BAC clone F24I3
C;Genetics:
A;Map position: 3
A;Introns: 104/3
A;Note: F24I3.50
C;Superfamily: Arabidopsis thaliana hypothetical protein F24I3.60
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47757

Query Match   12.0%; Score 73.5; DB 2; Length 253;
Best Local Similarity   27.1%; Pred. No. 7.5;
Matches 23; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

Qy   9 RLVAFTLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGID-------TLKNQTAH 61
        |: : : || |:||: :|:| |::|:|:
Db 156 KAVASYLSTVSATR---LGDNEWVQVSSSKIHNFSISNVLGGIEEDGFVLVDVSSSRSQ 212

Qy   62 GERAVDKLFQNLSLIKEHIERQKRC 86
        |::|:|:|||:|:|:|:||::|:||
Db 213 GE---RLFYTLHLQVENMDDYKINC 234

Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallor
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koerter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel,
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portatelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: G69698
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Molecule type: DNA
A;Residues: 1-1199 <KUN>
A;Cross-references: UNIPROT:P37871; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11884.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: rpoC
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta chain

Query Match   12.0%; Score 73; DB 2; Length 1199;
Best Local Similarity   34.7%; Pred. No. 51;
Matches 26; Conservative 12; Mismatches 31; Indels 6; Gaps 4;

Qy   35 TPENKNHQLCIKEVFQGIDTLKN--QTAHG-EAVDKLFQNLSLIKE--HIERQKRCAGE 89
        ||| : | : |:: :|::|:| | | :|:::|:
Db 142 TPLERKQLLSEKEYRAYLDKYGNKFQOASMGAERAIHKLLQDIDLVKEVDMLKEELKTSQGQ 201

Qy   - -RWRVTKFLDYLQVF 103
         |:| | | :|:|:|:
Db 202 RRTRAIKRLEVLEAF 216

RESULT 8
G69698
RNA polymerase (beta' subunit) rpoC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69698
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A;Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

RESULT 9
S33816
kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S33816
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:93267648; PMID:8496962
A;Accession: S33816
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-451 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L08258; NID:g161531; PID:g161532

Query Match   11.9%; Score 72.5; DB 2; Length 451;
Best Local Similarity   25.9%; Pred. No. 18;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

Qy   27 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGERAVDKLFQNLSLIKEHIERQKK 84
        |:|||:|:|:||:|||:| |||:|:|:|:||::|: :|:::|:||:|:|:|:||::|::|
Db   15 GQGNL-------SQEQIITGTREVIKGLBQLKNE--HNDIINSLYQSLRMLKKDTPGDSN 65

Qy   85 RCAGERWRVTKFLDYLQVFLG 105
        :|:|:|:|:|:|:|:|:||:|
Db   66 LVBEKTDIIEKSLESLELGLG 86

RESULT 10
S33813
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33813
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993

A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:9267648; PMID:8496962
A;Accession: S33813
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-649 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L10233; NID:g161525; PID:g161526

Query Match   11.9%; Score 72.5; DB 2; Length 649;
Best Local Similarity 25.9%; Pred. No. 28;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

Qy 27 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIRQKK 84
        ||| | :|| |: |||| |:|| ||
Db 15 GGGNL------------SQEQIITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy 85 RCAGERWRVTKFLDYLQVFLG 105
Db 66 LVEEKTDIIEKSLESLELGLG 86

RESULT 11
S33814
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33814
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:9267648; PMID:8496962
A;Accession: S33814
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-677 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L10234; NID:g161527; PID:g161528

Query Match   11.9%; Score 72.5; DB 2; Length 677;
Best Local Similarity 25.9%; Pred. No. 30;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

Qy 27 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIRQKK 84
Db 15 GGGNL------------SQEQIITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy 85 RCAGERWRVTKFLDYLQVFLG 105
Db 66 LVEEKTDIIEKSLESLELGLG 86

RESULT 12
S33815
kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S33815; S36727
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A;Title: Sequences of sea urchin kinesin light chain isoforms.
A;Reference number: S33813; MUID:9267648; PMID:8496962
A;Accession: S33815
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-686 <WED>
A;Cross-references: UNIPROT:Q05090; EMBL:L10235
R;Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
submitted to the EMBL Data Library, February 1993
A;Reference number: S36727
A;Accession: S36727
A;Status: preliminary
A;Residues: 1-568, 'A', 570-686 <WE2>
A;Cross-references: EMBL:L10235; NID:g161529; PID:g161530

Query Match   11.9%; Score 72.5; DB 2; Length 649;
Best Local Similarity 25.9%; Pred. No. 28;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

Qy 27 GDGNLMIPTPENKNHQLC--IKEVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIRQKK 84
Db 15 GGGNL------------SQEQIITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

Qy 85 RCAGERWRVTKFLDYLQVFLG 105
Db 66 LVEEKTDIIEKSLESLELGLG 86

RESULT 13
S28653
hypothetical protein IS (insertion sequence ISM1) - Methanobrevibacter smithii
C;Species: Methanobrevibacter smithii
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S28653
A;Molecule type: DNA
A;Residues: 1-401 <HAM>
A;Cross-references: UNIPROT:P22344; EMBL:X02587; NID:g44519; PIDN:CAA26424.1; PID:g44520
Mol. Gen. Genet. 200, 47-59, 1985
R;Hamilton, P.T.; Reeve, J.N.
A;Title: Structure of genes and an insertion element in the methane producing archaeba
A;Reference number: S28653; MUID:85295498; PMID:2993814
A;Accession: S28653
C;Genetic:
C;Mobile element: insertion sequence ISM1
C;Superfamily: Methanobrevibacter smithii hypothetical protein IS (insertion sequence ISM

Query Match   11.8%; Score 72; DB 2; Length 401;
Best Local Similarity 21.7%; Pred. No. 18;
Matches 23; Conservative 18; Mismatches 33; Indels 32; Gaps 3;

Qy   6 PMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGID------TLKNQTA 60
Db 247 PMYRNVADEIEV------------------KHQLCIFHLFQTINHKJKVYCRNNKI 284

Qy 61 HGEAVDKLFQNLSLIKEHIRQKKRCAGERWRVTKFLDYLQVFLGV 106
Db 285 NGKQRDHIYENAQELKNCFRQNSKKEA------IEQFKQYLQKYTAI 325

RESULT 14
B69498
hypothetical protein AF1987 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: B69498
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.,
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69498
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-216 <KLE>
A;Cross-references: UNIPROT:O28292; GB:AE000966; GB:AE000782; NID:g2689289; PIDN:AAB89271

Query Match   11.6%; Score 71; DB 2; Length 216;
Best Local Similarity 30.6%; Pred. No. 11;
Matches 26; Conservative 20; Mismatches 29; Indels 10; Gaps 4;

Qy 27 GDGNLMIPTPENKNHQLCIKEVFQG-IDTLKNQTAHGEAVDKLFQNLSLIKEHIRQKKR 85
Db 119 GDSVEIPTPP------IKKVNEDKLEIIRALERRGGSVDSINKLIELVEGKLEQKKY 171

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Qy     86 CAGERWRVTKFLDYLQVFLGVINTE 110
          |:|  |::  |:  ||:  ||:  ||
Db    172 MA-QRARMSYHLNGLEED-GLVVTE 194
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RESULT 15
F84594
hypothetical protein At2g20890 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84594
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84594
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <STO>
A;Cross-references: UNIPROT:Q9SKT0; GB:AE002093; NID:g4454459; PIDN:AAD20906.1; GSPDB:GN
C;Genetics:
A;Gene: At2g20890
A;Map position: 2

Query Match   11.6%; Score 71; DB 2; Length 300;
Best Local Similarity   31.4%; Pred. No. 16;
Matches 27; Conservative 15; Mismatches 26; Indels 18; Gaps 5;

```
Qy     34 PTPENKNHQLCI-------KRVFQGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCA 87
          ||  :|      ::||:|  |:|     :|||||:|:|
Db    219 PTVLDK---LCASLNINKKSVDRDLDVVRN-----LLSKLVQAKELLKEYVEREKKK-Q 268
```

```
Qy     88 GERWRVTKFLDYLQVFLGVINTEWTP 113
          |||  :|  ::  |||||
Db    269 GERAQSQKANETISKCLG--DTLYNP 292
```

Search completed: August 4, 2005, 17:12:00
Job time : 23.6305 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: August 4, 2005, 16:50:50 ; Search time 104.378 Seconds
(without alignments)
564.193 Million cell updates/sec

Title: US-10-787-382-10
Perfect Score: 610
Sequence: 1 FAVENPMNRLVAETLTLLST..........FLDYLQVFLGVINTEWTPES 115

Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 100 summaries

Database : UniProt_03:*
        1: uniprot_sprot:*
        2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	610	100.0	134	1	IL5_CANFA	Q95J76 canis famil
2	563	92.3	118	2	Q9TV10	canis famil
3	510	83.6	134	1	IL5_FELCA	O77515 felis silve
4	505	82.8	134	2	Q9TSD7	felis silve
5	501	82.1	134	2	Q9MYM5	sus scrofa
6	494	81.0	134	2	O02699	sus scrofa
7	491	80.5	134	1	IL5_HORSE	equus cabal
8	487	79.8	132	1	IL5_BOVIN	bos taurus
9	382	62.6	134	2	P52173	saimiri sci
10	372	61.0	135	1	IL5_CAVPO	cavia porce
11	361	59.2	134	1	IL5_CERTO	cercocebus
12	358	58.7	132	1	IL5_MERUN	meriones un
13	356	58.4	134	1	IL5_HUMAN	homo sapien
14	354	58.0	132	1	IL5_SIGHI	sigmodon hi
15	352	57.7	134	1	IL5_MACMU	P48093 macaca mula
16	347	56.9	133	1	IL5_MOUSE	P04401 mus musculu
17	346	56.7	139	1	IL5_MACEU	Q9xt91 macropus eu
18	332	54.4	132	1	IL5_RAT	O08125 rattus norv
19	325	53.3	132	2	Q9R2C9	rattus norv
20	214	35.1	48	2	Q6PVS2	ovis aries
21	109.5	18.0	40	2	Q9XT92	sminthopsis
22	94.5	15.5	590	1	MP44_MYXVL	myxoma viru
23	80.5	13.2	452	2	Q9Q8Q1	ashbya goss
24	78.5	12.9	258	2	Q9M1K0	arabidopsis
25	77	12.6	487	2	Q7R8B3	plasmodium
26	76.5	12.5	158	2	Q96575	leucophaea
27	75	12.3	292	2	Q8PUD3	methanosarc
28	75	12.3	360	2	Q62M23	burkholderi
29	75	12.3	360	2	Q63S03	burkholderi
30	74.5	12.2	1232	1	ADDA_BACSU	P23478 bacillus su
31	74	12.1	355	2	Q72418	listeria mo
32	73.5	12.0	161	2	Q6IL05	drosophila
33	73.5	12.0	253	2	Q9M1K1	arabidopsis
34	73.5	12.0	248	2	Q7MV24	porphyromon
35	73	12.0	655	2	Q8RVR0	helianthus
36	73	12.0	623	2	Q7XRA1	oryza sativ
37	73	12.0	661	2	Q921P5	mus musculu
38	73	12.0	401	1	DHSA_MOUSE	Q8k2b3 mus musculu
39	73	12.0	1199	1	RPOC_BACSU	P37871 bacillus su
40	72.5	11.9	229	2	Q9CLF5	pasteurella
41	72.5	11.9	418	2	Q8SLN1	oryza sativ
42	72.5	11.9	611	2	Q8GWT4	arabidopsis
43	72.5	11.9	645	2	Q6M0A6	methanococc
44	72.5	11.9	686	1	KLC_STRPU	O50090 strongyloce
45	72	11.8	296	2	Q8TQV4	methanobrev
46	72	11.8	216	1	YI48_METSM	P22344 methanosarc
47	72	11.8	562	1	YJ87_ARCFU	Q7th69 lycoris pot
48	72	11.8	437	1	SECY_STRGB	Q59912 streptomyce
49	71.5	11.7	595	2	Q6CS00	kluyveromyc
50	71.5	11.7	823	2	Q9X206	drosophila
51	71.5	11.7	328	1	O28292	archaeoglob
52	71	11.6	302	2	Q9SKT0	arabidopsis
53	71	11.6	300	1	O83IU2	enterococcu
54	71	11.6	347	2	Q57527	haemophilus
55	71	11.6	480	2	P74390	synechocyst
56	71	11.6	446	1	P79065	schizosacch
57	71.5	11.6	461	1	TIP1_SCHPO	setaria ita
58	71	11.6	2321	1	Q947M6	setaria ita
59	71	11.6	224	2	Q7PYK6	anopheles g
60	70.5	11.6	320	2	Q8TSW7	methanosarc
61	70.5	11.6	340	2	Q6N9Z5	rhodopseudo
62	70.5	11.6	406	2	Q6IWP4	brachydanio
63	70.5	11.6	437	2	Q9FKR7	arabidopsis
64	70.5	11.6	533	2	HSLV_HELHP	helicobacte
65	70	11.5	613	2	O84LD6	chrysanthem
66	70	11.5	246	2	Q64DU4	uncultured
67	70	11.5	294	2	Q8PCA2	xanthomonas
68	70	11.5	313	2	Q6FMT0	candida gla
69	70	11.5	406	2	Q9D5Q3	mus musculu
70	70	11.5	120	1	Q8DJV2	synechococc
71	70	11.5	1104	2	Q7N6A1	photorhabdu
72	70	11.5	180	1	Q7Q4J4	anopheles g
73	70	11.5	623	2	Q6BW69	debaryomyce
74	70	11.5	814	2	Q6FIR9	candida gla
75	70	11.5	899	2	O66RP8	lolium mult
76	70	11.5	933	2	O04145	acetabulari
77	70	11.5	1103	2	Q7PXB5	anopheles g
78	70	11.5	1136	2	Q6XZH5	solanum tub
79	70	11.5	1136	2	Q6XZH6	solanum tub
80	70	11.5	1136	2	Q6XZH8	solanum tub
81	70	11.5	2321	2	O84TQ5	setaria ita
82	70	11.5	4189	2	Q6BL44	debaryomyce
83	69.5	11.4	120	2	Q9CV87	mus musculu
84	69.5	11.4	253	2	Q97DG5	clostridium
85	69.5	11.4	293	2	Q7XAB8	solanum tub
86	69.5	11.4	331	2	Q9KBV9	bacillus ha
87	69.5	11.4	454	2	Q9U0K2	plasmodium
88	69.5	11.4	676	2	Q7YKV5	mapania par
89	69.5	11.4	976	2	O13544	homo sapien
90	69.5	11.4	1113	2	Q9CNR7	pasteurella
91	69.5	11.4	1179	2	Q13545	homo sapien
92	69.5	11.4	1188	2	Q92835	homo sapien
93	69.5	11.4	1188	2	Q92656	homo sapien
94	69.5	11.4	1189	2	O00145	homo sapien
95	69.5	11.4	1189	2	Q9UE80	homo sapien
96	69.5	11.4	1191	2	Q61181	mus musculu
97	69.5	11.4	1191	2	Q9U4X0	plasmodium
98	69.5	11.4	2647	2	O81EB6	plasmodium
99	69.5	11.4	2651	2	O81BB6	plasmodium
100	69.5	11.4	2770	2	Q7YUE9	plasmodium
			2957	2	Q8WRS6	plasmodium

ALIGNMENTS

Q61l05 droophila
Q9m1k1 arabidopsis
Q7mv24 porphyromon
Q8rvr0 helianthus
Q7xra1 oryza sativ
Q921p5 mus musculu
Q8k2b3 mus musculu
P37871 bacillus su
Q9clf5 pasteurella
Q8sln1 oryza sativ
Q8tqv4 methanobrev
Q7th69 lycoris pot
Q59912 streptomyce
Q6cs00 kluyveronyc
Q9x206 drosophila
O28292 archaeoglob
Q9skt0 arabidopsis
O83iu2 enterococcu
Q57527 haemophilus
P74390 synechocyst
P79065 schizosacch
Q947m6 setaria ita
Q7pyk6 anopheles g
Q8tsw7 methanosarc
Q6n9z5 rhodopseudo
Q6iwp4 brachydanio
Q9fkr7 arabidopsis
Q7vjd3 helicobacte
O84ld6 chrysanthem
Q64du4 uncultured
Q8pca2 xanthomonas
Q6fmt0 candida gla
Q9d5q3 mus musculu
Q8djv2 synechococc
Q7n6a1 photorhabdu
Q7q4j4 anopheles g
Q6bw69 debaryomyce
Q6fir9 candida gla
O66rp8 lolium mult
O04145 acetabulari
Q7pxb5 anopheles g
Q6xzh5 solanum tub
Q6xzh6 solanum tub
Q6xzh8 solanum tub
O84tq5 setaria ita
Q6bl44 debaryomyce
Q9cv87 mus musculu
Q97dg5 clostridium
Q7xab8 solanum tub
Q9kbv9 bacillus ha
Q9u0k2 plasmodium
Q7ykv5 mapania par
O13544 homo sapien
Q9cnr7 pasteurella
Q13545 homo sapien
Q92835 homo sapien
Q92656 homo sapien
O00145 homo sapien
Q9ue80 homo sapien
Q61181 mus musculu
Q9u4x0 plasmodium
O81eb6 plasmodium
O81bb6 plasmodium
Q7yue9 plasmodium
Q8wr86 plasmodium

```
RESULT 1
ID   IL5_CANFA    STANDARD;    PRT;   134 AA.
AC   Q95J76;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUN-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21334408; PubMed=11440633; DOI=10.1089/107999001750277835;
RA   Yang S., Sellins K.S., Weber E., McCall C.;
RT   "Canine interleukin-5: molecular characterization of the gene and
RT   expression of biologically active recombinant protein.";
RL   J. Interferon Cytokine Res. 21:351-367(2001).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF331920; AAL10716.1; -.
DR   EMBL; AF331919; AAL10715.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     21       By similarity.
FT   CHAIN        22    134       Interleukin-5.
FT   DISULFID     63     63       Interchain (with C-105) (By similarity).
FT   DISULFID    105    105       Interchain (with C-63) (By similarity).
FT   CARBOHYD     76     76       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15307 MW;  003C8D94D6FF4C6 CRC64;

Query Match             100.0%;  Score 610;  DB 1;  Length 134;
Best Local Similarity   100.0%;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNQHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNQHQLCIKEVFQGIDTLKNQTA 79

Qy         61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 134


RESULT 2
ID   Q9TV10       PRELIMINARY;    PRT;   118 AA.
AC   Q9TV10;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin-5 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091133; AAD46991.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13507 MW;  36A55633D67C9568C CRC64;

Query Match              92.3%;  Score 563;  DB 2;  Length 118;
Best Local Similarity    93.7%;  Pred. No. 7.2e-49;
  Matches  104;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNQHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNQHQLCIKEVFQGIDTLKNQTA 67

Qy         61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEW 111
              |||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         68 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVMNTEW 118


RESULT 3
ID   IL5_FELCA    STANDARD;    PRT;   134 AA.
AC   O77515; O62740;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Harley R., Day M.J., Gruffydd-Jones T.J., Harbour D.A., Helps C.R.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 12-128 FROM N.A.
RA   Padrid P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RX   MEDLINE=98452719; PubMed=9781459;
RT   "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL   Am. J. Vet. Res. 59:1263-1269(1998).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   --------------------------------------------------------------------------
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Query Match              ... %;  Score ...;  DB 2;
Best Local Similarity    ... %;

Qy          1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNQHQLCIKEVFQGIDTLKNQTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENNQHQLCIKEVFQGIDTLKNQTA 67

Qy         61 HGEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEW 111
              ||||||||||||||||||||||||||| : |: ||:|||:|||||| ||||
Db         68 HGEAVDKLFQNLSLIKEHIERQKRCAGKKWKVTNFLNYLQLFLGVMNTEW 118
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CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AF025436; AAC64505.1; -.
DR   EMBL; AF051372; AAC05752.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL   1   19   By similarity.
FT   CHAIN   20   134   Interleukin-5.
FT   DISULFID   63   105   Interchain (with C-105) (By similarity).
FT   DISULFID   105   63   Interchain (with C-63) (By similarity).
FT   CARBOHYD   76   76   N-linked (GlcNAc...) (By similarity).
FT   CARBOHYD   90   90   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   104   104   N-linked (GlcNAc...) (Potential).
FT   CONFLICT   105   105   KC -> NF (in Ref. 2).
FT   CONFLICT   108   108   ERWR -> KKWK (in Ref. 2).
FT   CONFLICT   111   111   K -> N (in Ref. 2).
FT   CONFLICT   114   114   K -> N (in Ref. 2).
FT   CONFLICT   117   117   D -> N (in Ref. 2).
FT   CONFLICT   117   117   V -> F (in Ref. 2).
FT   CONFLICT   121   121   VI -> LL (in Ref. 2).
FT   CONFLICT   125   126
SQ   SEQUENCE   134 AA; 15224 MW; 87D18DB8F8CAC820 CRC64;

Query Match   83.6%; Score 510; DB 1; Length 134;
Best Local Similarity   84.2%; Pred. No. 1.8e-43;
Matches   96; Conservative   10; Mismatches   8; Indels   0; Gaps   0;

Qy   2 AVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIEEVFQGIDTLKNQTAH 61
               ||||||||||||||||||||||||||||||||||||||||:||||| ||||||||||| :|
Db   21 AVQSPMNRLVAETLALLSTHRTLLIGDGNLMIPTPEHNNHQLCIEBVFQGIDTLKNRTVP 80

Db   81 GDAVEKLFRNLSLIKEHIDROKKKCGGERWRVKKFLDYLQVFLGVINTEWTIE 133

RESULT 4

ID   Q9TSD7   PRELIMINARY;   PRT;   134 AA.
AC   Q9TSD7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin 5.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vandegrift E., Hughes K.J., O'Reilly K.L.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF068770; AAC27616.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
SQ   SEQUENCE   134 AA; 15176 MW; 9A18B78F8CAC820 CRC64;

Query Match   82.8%; Score 505; DB 2; Length 134;
Best Local Similarity   84.1%; Pred. No. 5.8e-43;
Matches   95; Conservative   10; Mismatches   8; Indels   0; Gaps   0;

Qy   2 AVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIEKVFQGIDTLKNQTAH 61
               ||:||||||||||||||||||||||||||||||||||| |||||:||||||||||||| :|

Db   21 AVQSPMNRLVAETLALLSTHRTLLIGDGNLMIPTPEHNNHQLCIEBVFQGIDTLKNRTVP 80

Db   81 GDAVEKLFRNLSLIKEHIDROKKKCGGERWRVKKFLDYLQVFLGVINTEWTIE 133

Qy   62 GEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

Db   81 GDAVEKLFRNLSLIKEHIDROKKKCGGERWRVKKFLDYLQVFLGVINTEWTMES 134

RESULT 5

ID   Q9MYM5   PRELIMINARY;   PRT;   134 AA.
AC   Q9MYM5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin-5.
GN   Name=IL-5;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,
RA   Heegaard P.M.H.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ010088; CAB70611.2; -.
DR   EMBL; AJ133452; CAB38328.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
SQ   SEQUENCE   134 AA; 15191 MW; B485562A028A899 CRC64;

Immunogenetics 51:59-64(2000).
RX   MEDLINE=20130134; PubMed=10663563;
RA   Sylvin H., Matvienko O., leonchiks A., Alving K., van der Ploeg I.;
RT   "Molecular cloning, expression, and purification of pig interleukin-
RT   5.";
RL   Immunogenetics 51:59-64(2000).

Query Match   82.1%; Score 501; DB 2; Length 134;
Best Local Similarity   85.1%; Pred. No. 1.5e-42;
Matches   97; Conservative   7; Mismatches   10; Indels   0; Gaps   0;

Qy   2 AVENPMNRLVAETLTLLSTHRTWLLIGDGNLMIPTPENKNHQLCIEKVFQGIDTLKNQTAH 61
               |||| ||||||||||||||||||||||||||||||||||||||||:||||||||||||||

Db   21 AVENTNRLVAETLTLLSIHRTLLIGDGNLMIPTPVHTNHQLCIEBVFQGIDTLKNQTAR 80

Qy   62 GEAVDKLFQNLSLIKEHIEROKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115

Db   81 GDAVEKLFQNLSLIKEYIDROKKNCGGERWRVTQFLDYLQVFLGVINTEWTMES 134

RESULT 6

ID   IL5_HORSE   STANDARD;   PRT;   134 AA.
AC   O02699;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vandergrift E.V., Horohov D.W.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Factor that induces terminal differentiation of late-
    developing B-cells to immunoglobulin secreting cells (By
    similarity).
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-5 family.
```

```
DR   EMBL; U91947; AAB51382.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL         1     19       By similarity.
FT   CHAIN         20    134       Interleukin-5.
FT   DISULFID      63     63       Interchain (with C-105) (By similarity).
FT   DISULFID     105    105       Interchain (with C-63) (By similarity).
FT   CARBOHYD      76     76       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD      90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15081 MW;  2914840E3E7A006D CRC64;

Query Match      81.0%;           Score 494; DB 1; Length 134;
Best Local Similarity  84.1%;     Pred. No. 7.5e-42;
Matches  95; Conservative  8; Mismatches 10; Indels  0; Gaps  0;

Qy    2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAH 61
          |||:||||||||||||:||||||||| |||||||||| |||||||||||||||||||||
Db   21 AVESPMRLVAETLTLLSTHRTLLIGDGNLMIPTPEHKNHQLCIEEVFQGIDTLKNQTVQ 80

Qy   62 GEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPE 114
          :|||||||||||||| :-:|| ||||||||| ||||||||||||||||||
Db   81 GDAVAKLFQNLSLIKGYIDLQKKRCCGGERWRVKQFLDYLQEFLGVINTEWTIE 133
```

RESULT 7

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ID   IL5_BOVIN      STANDARD;      PRT;   134 AA.
AC   P52173;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=97075944; PubMed=8918267; DOI=10.1016/0378-1119(96)00252-1;
RA   Mertens B., Gobright E., Seow H.F.;
RT   "The nucleotide sequence of the bovine interleukin-5-encoding cDNA.";
RL   Gene 176:273-274(1996).
-!- FUNCTION: Factor that induces terminal differentiation of late-
    developing B-cells to immunoglobulin secreting cells (By
    similarity).
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-5 family.
```

```
DR   EMBL; Z67872; CAA91779.1; -.
DR   PIR; JC5116; JC5116.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL         1     21       By similarity.
FT   CHAIN         22    134       Interleukin-5.
FT   DISULFID      63     63       Interchain (with C-105) (By similarity).
FT   DISULFID     105    105       Interchain (with C-63) (By similarity).
FT   CARBOHYD      76     76       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD      90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15229 MW;  0B3A2328EE7431F4 CRC64;

Query Match      80.5%;           Score 491; DB 1; Length 134;
Best Local Similarity  81.6%;     Pred. No. 1.5e-41;
Matches  93; Conservative 12; Mismatches  9; Indels  0; Gaps  0;

Qy    2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAH 61
          |||:||||||||||||:|||||| ||||||||||::|| |||||||||||||||||||
Db   21 AVESTMNRLVAETLTLLSSHRTLLIGDGNLMIPTPQHTNHQLCIEEVFQGIDTLKNQTAQ 80

Qy   62 GEAVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPE 115
          :|||||||||||||: :|| | |||||||| ||||||||||||||||||||
Db   81 GDAVCKIFQNLSLIKEYIDLQKRKCGGERWRVKQFLDYLQVFLGVINTEWTMES 134
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-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-5 family.
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RESULT 8

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ID   IL5_SHEEP      STANDARD;      PRT;   132 AA.
AC   Q28586;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Seow H.-F., McWaters P.G., Hurst L., Wood P.R.;
RT   "Cloning of ovine interleukin-5 cDNA.";
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bryson C.E., Viney E., Brandon M., Boyd A.W.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Factor that induces terminal differentiation of late-
    developing B-cells to immunoglobulin secreting cells (By
    similarity).
-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-5 family.
```

DR   EMBL; U17053; AAB60629.1; -.
DR   EMBL; U17052; AAB60629.1; JOINED.
DR   EMBL; U35038; AAC99991.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL   1   19   By similarity.
FT   CHAIN   20   132   Interleukin-5.
FT   DISULFID   61   61   Interchain (with C-103) (By similarity).
FT   DISULFID   103   103   Interchain (with C-61) (By similarity).
FT   CARBOHYD   74   74   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   88   88   N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   132 AA; 14974 MW; D783F2B720E249D9 CRC64;

Query Match   Best Local Similarity 80.7%; Score 487; DB 1; Length 132;
            79.8%; Pred. No. 3.7e-41;
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy   2 AVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAH 61
Db   19 AVESTMNRLVAETLTLLSTHQTLLIGDGNLMIPTPQHTNHQLCIEBVFQGIDTLKNQTAQ 78

Qy   62 GEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
Db   79 GDAVKKIFRNLSLIKEYIDLQKRKCGGERWRVKQFLDYLQVFLGVINTEWTMES 132

RESULT 9
Q8MKH1
ID   Q8MKH1   PRELIMINARY;   PRT;   134 AA.
AC   Q8MKH1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin-5.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA   Heraud J.M., Lavergne A., Kazanji M.;
RT   "Molecular cloning, characterization, and quantification of squirrel
RT   monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL   Immunogenetics 54:20-29(2002).
DR   EMBL; AF294756; AAK92043.1; -.
DR   HSSP; P05113; 1HUL.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD006721; Interleukin_5; 1.
SQ   SEQUENCE   134 AA; 15210 MW; EAFACCA5DB48767C CRC64;

Query Match   Best Local Similarity 68.2%; Score 382; DB 2; Length 134;
            62.6%; Pred. No. 1.5e-30;
Matches 75; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy   6 PMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGEAV 65
Db   25 PTSALVKETLALLSTHRTLLMVNETLRIPVPAHKNHQLCTEBIFQGIGTLENQTVQSSGV 84

Qy   66 DKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
Db   85 EKLFQNLSLIKEHIDRQKKKCGQERRRVKQFLDYLQBFLGVINTEWTMES 134

RESULT 10
IL5_CAVPO
ID   IL5_CAVPO   STANDARD;   PRT;   135 AA.
AC   O08987;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=Il5;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96289181; PubMed=8764226;
RA   Mansour M., Karmilowicz M., Hawrylik S.J., Nalcerio B., Angilly J.,
RA   Conklyn M.J., Lilly C.M., Drazen J.M., Lee S.B., Auperin D.D.,
RA   de Wet J.R., Cohan V.L., Showell H.J., Danley D.E.;
RT   "Production and characterization of guinea pig IL-5 in baculovirus-
RT   infected insect cells.";
RL   Am. J. Physiol. 270:L1002-L1007(1996).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC   developing B-cells to immunoglobulin secreting cells (By
CC   similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
DR   EMBL; U34588; AAB61357.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL   1   19   By similarity.
FT   CHAIN   20   135   Interleukin-5.
FT   DISULFID   64   64   Interchain (with C-106) (By similarity).
FT   DISULFID   106   106   Interchain (with C-64) (By similarity).
FT   CARBOHYD   48   48   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   77   77   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   91   91   N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   135 AA; 15291 MW; EB85252132F52731 CRC64;

Query Match   Best Local Similarity 61.0%; Score 372; DB 1; Length 135;
            61.0%; Pred. No. 1.5e-29;
Matches 74; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy   7 MNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGEAVD 66
Db   27 LRALVRETLLLLSTHRTLLKGNETLRISVPAHKNHQLCIEBIFQGIDTLKNQTTQGEALA 86

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Qy          67  KLFQNLSLIKEHIERQKKRCAGERWMRVTKFLDYLQVFLGVINTEWTPE  114
                    ||||||||:|:||||||||| |:||||||||| ||||||| |
Db          87  TLFQNLSLIKKHIDLQKQKCGEERRRVKQFLDYLQEFLAVINTEWTIE  134

RESULT 11
ID    IL5_CERTO             STANDARD;      PRT;    134 AA.
AC    P46685;
DT    01-NOV-1995 (Rel. 32, Created)
DT    01-NOV-1995 (Rel. 32, Last sequence update)
DT    05-JUL-2004 (Rel. 44, Last annotation update)
DE    Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE    (Eosinophil differentiation factor).
GN    Name=IL5;
OS    Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC    Cercopithecinae; Cercocebus.
OX    NCBI_TaxID=9531;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=96003435; PubMed=7561102;
RA    Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT    "Comparative sequence analysis of cytokine genes from human and
RT    nonhuman primates.";
RL    J. Immunol. 155:3946-3954(1995).
CC    -!- FUNCTION: Factor that induces terminal differentiation of late-
CC        developing B-cells to immunoglobulin secreting cells (By
CC        similarity).
CC    -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC    -!- SUBCELLULAR LOCATION: Secreted.
CC    -!- SIMILARITY: Belongs to the IL-5 family.
CC    --------------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; L26033; AAA99971.1; -.
DR    HSSP; P05113; 1HUL.
DR    InterPro; IPR009079; 4_helix_cytokine.
DR    InterPro; IPR000186; Interleukin_5.
DR    Pfam; PF02025; IL5; 1.
DR    PRINTS; PR00432; INTERLEUKIN5.
DR    ProDom; PD006721; Interleukin_5; 1.
KW    Cytokine; Glycoprotein; Growth factor; Signal.
FT    SIGNAL        1     19
FT    CHAIN        20    134       Interleukin-5.
FT    DISULFID     63     63       Interchain (with C-105) (By similarity).
FT    DISULFID    105    105       Interchain (with C-63) (By similarity).
FT    CARBOHYD     22     22       O-linked (By similarity).
FT    CARBOHYD     47     47       N-linked (GlcNAc...) (Potential).
FT    CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
SQ    SEQUENCE   134 AA;  15339 MW;  7BDD491C43798IED CRC64;

Query Match             59.2%;  Score 361;  DB 1;  Length 134;
Best Local Similarity   63.4%;  Pred. No. 1.9e-28;
      Matches   71;  Conservative   17;  Mismatches   24;  Indels    0;  Gaps    0;

Qy           4  ENPMNRLVAETLTLLLSTHRTWLIGDGNLMLPTPENKNHQLCIKSVFQGIDTLKNQTAHGE  63
                 || |||||||| |||||||||||||| | ||:||||||||| |||||||| ::
Db          23  EIPTSALVKETLTLLLSTHRTLLIGNETLRIPVPVHKHQLCTEIFQGIGTLRSQTLQGG  82

Qy          64  AVDKLFQNLSLIKEHIERQKKRCAGERWMRVTKFLDYLQVFLGVINTEWTPES  115
                :| |||||||||||||||:|||| |  ||  |:|| ||||:|:|||||||
Db          83  TVERLFKQNLSLIKKYIDGQKKKCGEERRVNQFLDYLQEFLGVMNTEWIIES  134
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RESULT 12
ID    IL5_MERUN             STANDARD;      PRT;    132 AA.
AC    Q62575;
DT    01-NOV-1997 (Rel. 35, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    05-JUL-2004 (Rel. 44, Last annotation update)
DE    Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE    (Eosinophil differentiation factor).
GN    Name=IL5;
OS    Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC    Meriones.
OX    NCBI_TaxID=10047;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Spleen;
RA    Mai Z., Klei T.R.;
RL    Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC    -!- FUNCTION: Factor that induces terminal differentiation of late-
CC        developing B-cells to immunoglobulin secreting cells (By
CC        similarity).
CC    -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC    -!- SUBCELLULAR LOCATION: Secreted.
CC    -!- SIMILARITY: Belongs to the IL-5 family.
CC    --------------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; L37780; AAA655675.1; -.
DR    HSSP; P05113; 1HUL.
DR    InterPro; IPR009079; 4_helix_cytokine.
DR    InterPro; IPR000186; Interleukin_5.
DR    Pfam; PF02025; IL5; 1.
DR    PRINTS; PR00432; INTERLEUKIN5.
DR    ProDom; PD006721; Interleukin_5; 1.
KW    Cytokine; Glycoprotein; Growth factor; Signal.
FT    SIGNAL        1     17       Potential.
FT    CHAIN        18    132       Interleukin-5.
FT    DISULFID     61     61       Interchain (with C-103) (By similarity).
FT    DISULFID    103    103       Interchain (with C-61) (By similarity).
FT    CARBOHYD     45     45       N-linked (GlcNAc...) (Potential).
FT    CARBOHYD     74     74       N-linked (GlcNAc...) (Potential).
FT    CARBOHYD     88     88       N-linked (GlcNAc...) (Potential).
SQ    SEQUENCE   132 AA;  15164 MW;  60CB3852F9F84261 CRC64;

Query Match             58.7%;  Score 358;  DB 1;  Length 132;
Best Local Similarity   61.1%;  Pred. No. 3.8e-28;
      Matches   69;  Conservative   18;  Mismatches   26;  Indels    0;  Gaps    0;

Qy           2  AVENPMNRLVAETLTLLLSTHRTWLIIGDGNLMLPTPENKNHQLCIKRVFQGIDTLKNQTAH  61
                 |:| |||| |||||||||||||||||:|||| | ||:||||||||||:|:||||||||| |
Db          19  ALEIPMSAVVKETLIQLSTHRALITSNETVRLPVPTHKHQLCIGEIFQGLDILKNQTAR  78

Qy          62  GEAVDKLFQNLSLIKEHIERQKKRCAGERWMRVTKFLDYLQVFLGVINTEWTPE  114
                |:  | ||||||||||||::|||| || || | |:|| ||||:|:|||||||
Db          79  GGAVETLFQNLSLIKKYIDRQKRKCGEERRRAROFLDYLQEFLGVMSTEWTME  131
```

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RESULT 13
ID    IL5_HUMAN             STANDARD;      PRT;    134 AA.
AC    P05113; Q13840;
DT    13-AUG-1987 (Rel. 05, Created)
DT    13-AUG-1987 (Rel. 05, Last sequence update)
DT    25-OCT-2004 (Rel. 45, Last annotation update)
DE    Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
```

```
DE   (Eosinophil differentiation factor) (B cell differentiation factor I).
GN   Name=IL5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87066782; PubMed=3024129;
RA   Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,
RA   Yaoita Y., Takatsu K., Hammarstroem L., Smith C.I.E., Severinson E.,
RA   Honjo T.;
RT   "Cloning of cDNA for human T-cell replacing factor (interleukin-5) and
RT   comparison with the murine homologue.";
RL   Nucleic Acids Res. 14:9149-9158(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88059042; PubMed=2824500;
RA   Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;
RT   "Molecular cloning and structure of the human interleukin-5 gene.";
RL   J. Biol. Chem. 262:16580-16584(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88016145; PubMed=3498940;
RA   Campbell H.D., Tucker W.Q.J., Hort Y., Martinson M.E., Mayo G.,
RA   Clutterbuck E.J., Sanderson C.J., Young I.G.;
RT   "Molecular cloning, nucleotide sequence, and expression of the gene
RT   encoding human eosinophil differentiation factor (interleukin 5).";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88041112; PubMed=2822259;
RA   Yokota T., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,
RA   Yokota K., Gemmell L., Shrader B., Yang G., Meyerson P., Luh J.,
RA   Hoy P., Pene J., Briere F., Spits H., Banchereau J., de Vries J.,
RA   Lee F.D., Arai N., Arai K.;
RT   "Isolation and characterization of lymphokine cDNA clones encoding
RT   mouse and human IgA-enhancing factor and eosinophil colony-stimulating
RT   factor activities; relationship to interleukin 5.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Honjo T., Takatsu K., Severinson E.;
RL   Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 20-134, AND DISULFIDE BONDS.
RX   MEDLINE=90299868; PubMed=2361960;
RA   Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,
RA   Tsujimoto M.;
RT   "Structure of recombinant human interleukin 5 produced by Chinese
RT   hamster ovary cells.";
RL   J. Biochem. 107:292-297(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX   MEDLINE=93247642; PubMed=8435502; DOI=10.1038/363172a0;
RA   Milburn M.V., Hasell A.M., Lambert M.H., Jordan S.R.,
RA   Proudfoot A.E.I., Graber P., Wells T.N.C.;
RT   "A novel dimer configuration revealed by the crystal structure of human
RT   interleukin-5.";
RL   Nature 363:172-176(1993).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   -!- DATABASE: NAME=R&d Systems' cytokine mini-reviews; IL5;
CC       WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=207".
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X04688; CAA28390.1; -.
DR   EMBL; J03478; AAA74469.1; -.
DR   EMBL; J02971; AAA98620.1; -.
DR   EMBL; X12705; CAA31210.1; -.
DR   EMBL; X12705; CAA31210.1; -.
DR   EMBL; X12706; CAA31211.1; -.
DR   EMBL; AF353265; AAK19759.1; -.
DR   PIR; A28477; A28477.
DR   PDB; 1HUL; X-ray; A/B=24-131.
DR   Genew; HGNC:6016; IL5.
DR   MIM; 147850; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0005137; F:interleukin-5 receptor binding; TAS.
DR   GO; GO:0009626; P:hypersensitive response; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR000186; Interleukin_5.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKIN5.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;
KW   Growth factor; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    134       Interleukin-5.
FT   DISULFID     63     63       Interchain (with C-105).
FT   DISULFID    105    105       Interchain (with C-63).
FT   CARBOHYD     22     22       O-linked.
FT   CARBOHYD     47     47       N-linked (GlcNAc...).
FT   CONFLICT     88     88       F -> L (in Ref. 5; CAA31210).
FT   HELIX        26     38
FT   TURN         39     40
FT   HELIX        41     45
FT   TURN         46     46
FT   STRAND       51     54
FT   HELIX        60     62
FT   HELIX        64     77
FT   TURN         82     82
FT   HELIX        83    103
FT   TURN        104    105
FT   STRAND      108    111
FT   TURN        112    128
FT   HELIX       129    129
SQ   SEQUENCE   134 AA;  15238 MW;  DC98446717955EA3 CRC64;

Query Match             58.4%;  Score 356;  DB 1;  Length 134;
Best Local Similarity   62.5%;  Pred. No. 6.1e-28;
Matches   70;  Conservative   16;  Mismatches   26;  Indels    0;  Gaps    0;

Qy    4 ENPMNRIVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGIDTLKNQTAHGE 63
         | :||:|||||||:|:||| |:||:||||||:|||:|||:|||||||||:||:||||||
Db   23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG 82

Qy   64 AVDKLFQNLSLIKEHIERQKRCAGERWRVTKFLDYLQVFLGVINTEWTPES 115
         |:|:||||||||||||||:|:|||||||||||||||||||||||||||
Db   83 TVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWIIES 134
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RESULT 14
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ID   IL5_SIGHI     STANDARD;     PRT;   132 AA.
AC   Q9ESI9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   PubMed=11054577; DOI=10.1016/S0378-1119(00)00366-8;
RA   Howard S., Jacquet A., Haumont M., Milican F., Glineur F.,
RA   Bollen A.;
RT   "Cloning, expression and purification of recombinant cotton rat
RT   interleukin-5.";
RL   Gene 257:149-155(2000).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   -!--------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -!--------------------------------------------------------------------------
DR   EMBL; AF142211; AAG16722.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     19       By similarity.
FT   CHAIN        20    132       Interleukin-5.
FT   DISULFID     61     61       Interchain (with C-103) (By similarity).
FT   DISULFID    103    103       Interchain (with C-61) (By similarity).
FT   CARBOHYD     45     45       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     74     74       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     88     88       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   132 AA;  15434 MW;  B32B8B1B2371FEB9 CRC64;

Query Match          58.0%;  Score 354;  DB 1;  Length 132;
Best Local Similarity 59.6%;
Matches  68;  Conservative  17;  Mismatches  29;  Indels  0;  Gaps  0;

Qy    1  FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGITLKNQTA   60
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Db   18  FAVEIPMHTVVKETLIQLSTHRALLTSNETVRLPVPTHKNHQLCIGRIFRGLDILKNQTV   77

Qy   61  HGEAVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPE   114
         :|  ||||FQNLSLIK :|:|||:|:C | |||  :|||||||| ||| |||| |
Db   78  RGGTVETLFQNLSLIKKYIDRQKEKCGEERRTRQFLDYLQEFLGVWGTEWTME   131
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RESULT 15
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ID   IL5_MACMU     STANDARD;     PRT;   134 AA.
AC   P48093;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE   (Eosinophil differentiation factor).
GN   Name=IL5;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: Factor that induces terminal differentiation of late-
CC       developing B-cells to immunoglobulin secreting cells (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-5 family.
CC   -!--------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -!--------------------------------------------------------------------------
DR   EMBL; U19848; AAA86710.1; -.
DR   HSSP; P05113; 1HUL.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000186; Interleukin_5.
DR   Pfam; PF02025; IL5; 1.
DR   PRINTS; PR00432; INTERLEUKINS.
DR   ProDom; PD006721; Interleukin_5; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     19       By similarity.
FT   CHAIN        20    134       Interleukin-5.
FT   DISULFID     63     63       Interchain (with C-105) (By similarity).
FT   DISULFID    105    105       Interchain (with C-63) (By similarity).
FT   CARBOHYD     22     22       O-linked (By similarity).
FT   CARBOHYD     47     47       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     90     90       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   134 AA;  15150 MW;  DC985ECF4BAB86A3 CRC64;

Query Match          57.7%;  Score 352;  DB 1;  Length 134;
Best Local Similarity 62.5%;
Matches  70;  Conservative  15;  Mismatches  27;  Indels  0;  Gaps  0;

Qy    4  ENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFQGITLKNQTAHGE   63
         : | ::|| | |:|||||||| || |:|| | :  |:|||| | : |||||||:.||  |
Db   23  BIPASALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGITLRSQTVQGG   82

Qy   64  AVDKLFQNLSLIKEHIERQKKRCAGERWRVTKFLDYLQVFLGVINTEWTPES  115
         :| :LFQNLSLIK : :|:|||:C |  |||  :|||||||| |||: ||| |
Db   83  TVERLFQNLSLIKYIGGQKKKCGEBRRVNQFLDYLQEFLGVWNTEWIIES  134
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Search completed: August 4, 2005, 17:11:06
Job time : 105.378 secs

OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: August 6, 2005, 20:22:55 ; Search time 118.932 Seconds
                                            (without alignments)
                                            1843.588 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLLNLSLLALGAAYVSAF..........FLDYLQVPLGVINTEWTPES 134

Scoring table: BLOSUM62
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                Ygapop 10.0 ; Ygapext 0.5
                Pgapop   6.0 ; Pgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10787382/runat_04082005_084753_19321/app_query.fasta_1.590
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-MOBE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued Patents NA:*
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          2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
          3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
          4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
          5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
          6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

SUMMARIES

Result No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	696	100.0	402	4	US-09-322-409-83	Sequence 83, Appl
2	696	100.0	402	4	US-09-322-409-84	Sequence 84, Appl
c 3	696	100.0	402	4	US-09-451-527-83	Sequence 83, Appl
c 4	696	100.0	402	4	US-09-451-527-84	Sequence 84, Appl
c 5	696	100.0	610	4	US-09-322-409-80	Sequence 80, Appl
c 6	696	100.0	610	4	US-09-322-409-82	Sequence 82, Appl
c 7	696	100.0	610	4	US-09-451-527-80	Sequence 80, Appl
c 8	696	100.0	610	4	US-09-451-527-82	Sequence 82, Appl
c 9	687	98.7	405	4	US-09-371-615A-1	Sequence 1, Appli
c 10	610	87.6	345	4	US-09-322-409-85	Sequence 85, Appl
c 11	610	87.6	345	4	US-09-451-527-85	Sequence 85, Appl
c 12	610	87.6	345	4	US-09-451-527-85	Sequence 85, Appl

c	13	610	87.6	345	4	US-09-451-527-87	Sequence 87, Appl
c	14	430	61.8	816	3	US-09-079-839-2	Sequence 2, Ap
c	15	424	60.9	816	4	US-09-023-655-1236	Sequence 1236, Ap
c	16	376	54.0	1534	3	US-08-629-643A-4	Sequence 4, Appl
c	17	376	54.0	1534	3	US-09-155-884-4	Sequence 4, Appl
c	18	351	50.4	377	3	US-09-180-864-1	Sequence 1, Appli
c	19	332.5	47.8	381	4	US-09-556-818-27	Sequence 27, Appl
c	20	331.5	47.6	399	4	US-09-556-818-39	Sequence 39, Appl
c	21	330.5	47.5	375	4	US-09-556-818-33	Sequence 33, Appl
c	22	328.5	47.2	393	4	US-09-556-818-31	Sequence 31, Appl
c	23	324	46.6	444	4	US-09-556-818-43	Sequence 43, Appl
c	24	322.5	46.3	393	4	US-09-556-818-41	Sequence 41, Appl
c	25	321.5	46.2	375	4	US-09-556-818-37	Sequence 37, Appl
c	26	319.5	45.9	375	4	US-09-556-818-45	Sequence 45, Appl
c	27	318.5	45.8	393	4	US-09-556-818-55	Sequence 55, Appl
c	28	315.5	45.3	387	4	US-09-556-818-49	Sequence 49, Appl
c	29	311	44.7	438	4	US-09-556-818-59	Sequence 59, Appl
c	30	309.5	44.5	387	4	US-09-556-818-57	Sequence 57, Appl
c	31	308.5	44.3	369	4	US-09-556-818-53	Sequence 53, Appl
c	32	301.5	43.3	357	4	US-09-556-818-35	Sequence 35, Appl
c	33	299.5	43.0	375	4	US-09-556-818-29	Sequence 29, Appl
c	34	289.5	41.6	351	4	US-09-556-818-51	Sequence 51, Appl
c	35	287.5	41.3	369	4	US-09-556-818-47	Sequence 47, Appl
c	36	222	31.9	6727	3	US-08-629-643A-5	Sequence 5, Appli
c	37	222	31.9	6727	3	US-09-280-799-1	Sequence 1, Appli
c	38	222	31.9	6727	3	US-08-629-643A-5	Sequence 5, Appli
c	39	215.5	31.0	3230	3	US-09-155-884-5	Sequence 5, Appli
c	40	215.5	31.0	3230	6	US-09-280-799-78	Sequence 78, Appl
c	41	215.5	31.0	3230	6	US-09-280-799-78	Sequence 78, Appl
c	42	76	10.9	33140	4	US-09-596-002-23	Sequence 23, Appl
c	43	75.5	10.8	4964	4	US-09-799-451-475	Sequence 475, App
c	44	75	10.8	57	4	US-09-556-810-61	Sequence 61, Appl
c	45	75	10.8	79595	4	US-09-949-016-15318	Sequence 15318, A

ALIGNMENTS

RESULT 1
US-09-322-409-83

; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 83
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-322-409-83

Alignment Scores:
Pred. No.:   3.15e-93
Score: 696.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB:

Length: 402
Matches: 134
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
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US-10-787-382-5 (1-134) x US-09-322-409-83 (1-402)

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Qy       1 ATGAGAAATGCTTCTGAAATTGGAGTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTCCTTT 60

Qy      21 AlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuSerThrHis 40
Qy      61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

Db      41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db     121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 180

Qy      61 GlyLeuCysIleLysGluValPheGlyIleAspThrLeuLysGlnThrArgAlaHis 80
Qy     181 CAACCTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC 240

Db      81 GlyGluValAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleIleGluArg 100
Db     241 GGGGAGGCTGTGGGCATAAACTATTCCAAAACTGTCTTAATAAAAGAACACATAGAGCGC 300

Qy     101 GlnLysLysArgCysAlaGlyLysArgTrpArgValThrLysSerPheLeuAspTyrLeuGln 120
Qy     301 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360

Qy     121 ValPheLeuGlyValAlaIleAsnThrGlnThrTrpThrProGluSer 134
Qy     361 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAAGT 402

DB: US-09-322-409-84

RESULT 2
US-09-322-409-84//c
; Sequence 84, Application US//09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris

Alignment Scores:
Pred. No.:
Score:             3.15e-93        Length:          402
Percent Similarity: 696.00         Matches:         134
Best Local Similarity: 100.00%     Conservative:    0
Query Match:       100.00%         Mismatches:      0
DB:                4               Indels:          0
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US-10-787-382-5 (1-134) x US-09-322-409-84 (1-402)

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Db       1 ATGAGAAATGCTTCTGAAATTGGAGTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTCCTTT 343

Qy      21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
Db     342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

Qy      41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db     282 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 223

Qy      61 GlnLeuCysIleLysGluValPheGlyIleAspThrLeuLysGlnThrArgAlaHis 80
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Db     222 CAACCTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCAC 163

Qy      81 GlyGluValAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleIleGluArg 100
Db     162 GGGGAGGCTGTGGGCATAAACTATTCCAAAACTGTCTTAATAAAAGAACACATAGAGCGC 103

Qy     101 GlnLysLysArgCysAlaGlyLysArgTrpArgValThrLysSerPheLeuAspTyrLeuGln 120
Db     102 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 43

Qy     121 ValPheLeuGlyValAlaIleAsnThrGlnThrTrpThrProGluSer 134
Db      42 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAAGT 1

RESULT 3
US-09-451-527-83
; Sequence 83, Application US//09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris

Alignment Scores:
Pred. No.:
Score:             3.15e-93        Length:          402
Percent Similarity: 696.00         Matches:         134
Best Local Similarity: 100.00%     Conservative:    0
Query Match:       100.00%         Mismatches:      0
DB:                4               Indels:          0
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US-10-787-382-5 (1-134) x US-09-451-527-83 (1-402)

Qy       1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
Db       1 ATGAGAAATGCTTCTGAAATTGGAGTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTCCTTT 60

Qy      21 AlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuSerThrHis 40
Db      61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

Qy      41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
Db     121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 180

Qy      61 GlnLeuCysIleLysGluValPheGlyIleAspThrLeuLysGlnThrArgAlaHis 80
Db     181 CAACCTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCAC 240

Qy      81 GlyGluValAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleIleGluArg 100
Db     241 GGGGAGGCTGTGGGCATAAACTATTCCAAAACTGTCTTAATAAAAGAACACATAGAGCGC 300

Qy     101 GlnLysLysArgCysAlaGlyLysArgTrpArgValThrLysSerPheLeuAspTyrLeuGln 120
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Db  301 CAAAAAAAAGGTGTGCAGGAGAGATGACAAAGTTCCTAGACTACCTGCA 360
Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Db  361 GTATTTCTTGGTGTAATAAACACCGAGTGGACCCGAAAGT 402
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RESULT 4
US-09-451-527-84/c
; Sequence 84, Application US/09451527
; Patent No. 6482403
GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shunin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84

Alignment Scores:
Pred. No.:
Score: 3.15e-93
Percent Similarity: 696.00   Length: 402
Best Local Similarity: 100.00%   Matches: 134
Query Match: 100.00%   Conservative: 0
                                       Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-84 (1-402)

Qy   1 MetArgThrMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
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Db   1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGCCTATAGTTTCTGCCTTT 343

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACTCAT 283

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluLysLysAsnHis 60
          ||||||||||||||||||||||||||||||||||||||||||||
Db 282 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAAAATCAC 223

Qy   61 GlnLeuCysIleLysGlyValPheGlnGlyIleLysAspThrLeuLysAsnGlnThrAlaHis 80
          |||||||||||||||||||||||||||||||||||||||
Db 222 CAACTGTGCATTAAAGAAGGTATTTTCAGGGTATAAAGACCAAACTGCCAC 163

Qy   81 GlyGluAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 162 GGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAAGAACACATAGAGGC 103

Qy 101 GlnLeuLysLysArgCysAlaLeuGlyAlaArgValThrLysPheLeuAspTyrLeuGln 120
          ||||||||||||||||||||||||||||||||||||||||||
Db 102 CAAAAAAAAGGTGTGCAGGAGAGATGACAAAGTTCCTAGACTACCTGCAA 43

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Db   42 GTATTTCTTGGTGTAATAAACACCGAGTGGACCCGAAAGT 1
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RESULT 5
US-09-322-409-80
; Sequence 80, Application US/0932409

; Patent No. 6471957
GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-322-409-80

Alignment Scores:
Pred. No.:
Score:                  6.03e-93
Percent Similarity:     696.00         Length:       610
Best Local Similarity:  100.00%        Matches:      134
Query Match:            100.00%        Conservative: 0
                                       Mismatches:   0
                                       Indels:       0
                                       Gaps:         0

US-10-787-382-5 (1-134) x US-09-322-409-80 (1-610)

Qy    1 MetArgThrMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGCCTATAGTTTCTGCCTTT 88

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACTCAT 148

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluLysLysAsnHis 60
          ||||||||||||||||||||||||||||||||||||||||||||
Db  149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAAAATCAC 208

Qy   61 GlnLeuCysIleLysGlyValPheGlnGlyIleLysAspThrLeuLysAsnGlnThrAlaHis 80
          |||||||||||||||||||||||||||||||||||||||
Db  209 CAACTGTGCATTAAAGAAGGTATTTTCAGGGTATAAAGACCAAACTGCCAC 268

Qy   81 GlyGluAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  269 GGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAAGAACACATAGAGGC 328

Qy  101 GlnLeuLysLysArgCysAlaLeuGlyAlaArgValThrLysPheLeuAspTyrLeuGln 120
          ||||||||||||||||||||||||||||||||||||||||||
Db  329 CAAAAAAAAGGTGTGCAGGAGAGATGACAAAGTTCCTAGACTACCTGCAA 388

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
          ||||||||||||||||||||||||||||||
Db  389 GTATTTCTTGGTGTAATAAACACCGAGTGGACCCGAAAGT 430
```

RESULT 6
US-09-322-409-82/c
; Sequence 82, Application US/09322409
; Patent No. 6471957
GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-82

Alignment Scores:
Pred. No.:
Score: 6.03e-93   Length: 610
Percent Similarity: 696.00   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                       Gaps: 0

US-10-787-382-5 (1-134) x US-09-322-409-82 (1-610)

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Qy    1 MetArgMetLeuLeuLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
Db  582 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGGCTTGACACTGTTTCTGCCTTT      523

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis            40
Db  522 GCTGTGGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT          463

Qy   41 ArgThrThrLeuLeuIleGlyTyrAspGlyAsnLeuMetIleProThrHisProGluAsnLysAsnHis  60
Db  462 CGAACTACGGTTGATAGGGCGATGGGAACCTACTCCTGAAAATAAAAATCAC                  403

Qy   61 GlnLeuCysIleLeuLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis     80
Db  402 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC        343

Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg        100
Db  342 GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTAATAAAAGAACACAATAGAGCGC         283

Qy  101 GlnLeuLysArgGlyValGluArgValThrLysPheLeuAspTyrLeuGln                   120
Db  282 CAAAAAAAAGGTGTGCAGGAGAGAAGATGGAGAGTCGACAAAGTTCCTAGACTACCTGCAA        223

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                            134
Db  222 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGAAAGT                            181
```

RESULT 7
US-09-451-527-80
; Sequence 80, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THERBOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610

; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-451-527-80

Alignment Scores:
Pred. No.:
Score: 6.03e-93   Length: 610
Percent Similarity: 696.00   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                       Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-80 (1-610)

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Qy    1 MetArgMetLeuLeuLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
Db   89 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGGCTTGACACTGTTTCTGCCTTT      88

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis            40
Db  149 GCTGTGGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT          148

Qy   41 ArgThrThrLeuLeuIleGlyTyrAspGlyAsnLeuMetIleProThrHisProGluAsnLysAsnHis  60
Db  149 CGAACTACGGTTGATAGGGCGATGGGAACCTACTCCTGAAAATAAAAATCAC                  208

Qy   61 GlnLeuCysIleLeuLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis     80
Db  209 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC        268

Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg        100
Db  269 GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTAATAAAAGAACACAATAGAGCGC         328

Qy  101 GlnLeuLysArgGlyValGluArgValThrLysPheLeuAspTyrLeuGln                   120
Db  329 CAAAAAAAAGGTGTGCAGGAGAGAAGATGGAGAGTCGACAAAGTTCCTAGACTACCTGCAA        388

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                            134
Db  389 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGAAAGT                            430
```

RESULT 8
US-09-451-527-82/c
; Sequence 82, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THERBOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-82

Alignment Scores:
Pred. No.:   6.03e-93   Length: 610

Score: 696.00   Matches: 134
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 4   Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-82 (1-610)

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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  582  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTTAGTTTCTGCCTTT  523

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis  40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  522  GCTGTGGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT  463

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  462  CGAACCTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC  403

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis  80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  402  CAACCTGCATTAAAGGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCCAC  343

Qy   81  GlyGluValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleIleGluArg  100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  342  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC  283

Qy  101  GlnLysGlyArgCysSerLeuGlyArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  282  CAAAAAAAAGGGTGTCGACTAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA  223

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
         |||||||||||||||||||||||||||||||||||
Db  222  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGAAAGT  181
```

RESULT 9
US-09-371-615A-1
; Sequence 1, Application US/0937161SA
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1

Alignment Scores:
Pred. No.:
Score: 687.00   Length: 405
Percent Similarity: 99.25%   Matches: 133
Best Local Similarity: 99.25%   Conservative: 0
Query Match: 98.71%   Mismatches: 1
DB: 4   Indels: 0
                                Gaps: 0

US-10-787-382-5 (1-134) x US-09-371-615A-1 (1-405)

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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTTAGTTTCTGCCTTT  60

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis  40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT  120
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RESULT 10
US-09-322-409-85
; Sequence 85, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-322-409-85

Alignment Scores:
Pred. No.:
Score: 610.00   Length: 345
Percent Similarity: 100.00%   Matches: 115
Best Local Similarity: 100.00% Conservative: 0
Query Match: 87.64%   Mismatches: 0
DB: 4   Indels: 0
                                Gaps: 0

US-10-787-382-5 (1-134) x US-09-322-409-85 (1-345)

```
Qy   20  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr  39
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  60

Qy   40  HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  59
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CATCGAACCTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT  120

Qy   60  HisGlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAla  79
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CACCAACTGTGCATTAAAGGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC  180

Qy   80  HisGlyGluValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu  99
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CACGGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG  240
```

```
Qy  100  ArgGlnLysArgCysAlaGlyGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu   119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CGCCAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG    300

Qy  120  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
              |||||||||||||||||||||||||||||||||||||||||
Db  301  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT   345
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RESULT 11
US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87

Alignment Scores:
Pred. No.:
Score: 1.25e-80   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 87.64%   Indels: 0
                                4   Gaps: 0

US-10-787-382-5 (1-134) x US-09-322-409-87 (1-345)

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Qy   20  PheAlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuLeuSerThr   39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGGAGACCTTGACACTGCTCTCCACT    286

Qy   40  HisArgThrArgLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsn   59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  285  CATCGAACTCGGCTGATAGGCGGAACCTGATGATTCCTACTCCCTGAAAATAAAAAT        226

Qy   60  HisGlnLeuCysIleGlyLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla   79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  225  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC    166

Qy   80  HisGlyGluAlaAlaAspLysLeuPheGlnAsnLeuSerLeuIleGlyGluHisIleGlu   99
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  165  CACCGGCGAGGCTGCTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG  106

Qy  100  ArgGlnLysArgCysAlaGlyGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu   119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  105  CGCCAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG     46

Qy  120  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
              |||||||||||||||||||||||||||||||||||||||||
Db   45  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT     1
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RESULT 12
US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

Alignment Scores:
Pred. No.:
Score: 1.25e-80   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 87.64%   Indels: 0
                                4   Gaps: 0

US-10-787-382-5 (1-134) x US-09-451-527-85 (1-345)

```
Qy   20  PheAlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuLeuSerThr   39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGGAGACCTTGACACTGCTCTCCACT     60

Qy   40  HisArgThrArgLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsn   59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CATCGAACTCGGCTGATAGGCGGAACCTGATGATTCCTACTCCCTGAAAATAAAAAT        120

Qy   60  HisGlnLeuCysIleGlyLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla   79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC    180

Qy   80  HisGlyGluAlaAlaAspLysLeuPheGlnAsnLeuSerLeuIleGlyGluHisIleGlu   99
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CACCGGCGAGGCTGCTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG  240

Qy  100  ArgGlnLysArgCysAlaGlyGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu   119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  CGCCAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG    300

Qy  120  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
              |||||||||||||||||||||||||||||||||||||||||
Db  301  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT   345
```

RESULT 13
US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306

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;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 87
;   LENGTH: 345
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-451-527-87

Alignment Scores:
Pred. No.:                1.25e-80
Score:                    610.00
Percent Similarity:       100.00%
Best Local Similarity:    100.00%
Query Match:              87.64%
DB:

                          Length:         345
                          Matches:        115
                          Conservative:   0
                          Mismatches:     0
                          Indels:         0
                          Gaps:           0

US-10-787-382-5 (1-134) x US-09-451-527-87 (1-345)

Qy     20  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr   39
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Db    225  CACCAACTGTCCATTAAAGAAGTTTTTCAGGGATGTATACAGACACAT          166

Qy     40  HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn   59
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               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285  CATCGAACTTGGCTGATAGGCGGATGGGGAACCTGATGATTCCTACTCCTGAAAATAAAAT  226

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Db    225  CACCAACTGTCCATTAAAGAAGTTTTTCAGGGATGTATACAGACACATTGAAGAACCAAACTGCC  166

Qy     80  HisGlyGluAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGlu   99
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    100  ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrArgPheLeuAspTyrLeu  119
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Qy    120  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
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RESULT 14
US-09-079-839-2
;   Sequence 2, Application US/0907983
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;   Patent No. 6048726
;   GENERAL INFORMATION:
;   APPLICANT: Weltman, Joel K.
;   APPLICANT: Karim, Aftab S.
;   TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION
;   FILE REFERENCE: 09998/002001
;   CURRENT APPLICATION NUMBER: US/09/079,839
;   CURRENT FILING DATE: 1998-05-15
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: FastSEQ for Windows Version 3.0
;
;   SEQ ID NO 2
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-079-839-2

Alignment Scores:
Pred. No.:                1.83e-53
Score:                    430.00
Percent Similarity:       77.61%
Best Local Similarity:    64.93%
Query Match:              61.78%
DB:

                          Length:         816
                          Matches:        87
                          Conservative:   17
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                          Indels:         0
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US-10-787-382-5 (1-134) x US-09-079-839-2 (1-816)

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Right column:

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Qy     41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
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Db    165  CGAACTCTGCTGATAGGCCAATGAGACTCGAGGAATTCCTGTACATAAAAAATCAC  224

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Qy     81  GlyGluAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
               |||   :::|||||||   ||||||||||||:::::::||:::::|||
Db    285  GGGGGTACTGTCGAAAAGACTATTCAAAAACTTGTCCTTAATAAGAAATACAATTGACGGC  344

Qy    101  GlnLysLysArgCysAlaGlyGluArgTrpArgValThrArgPheLeuAspTyrLeuGln  120
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Db    345  CAAAAAAAAAAAGTGTGGAGAAGACGGGAGTAAACCAATTCCTAGACTACCTGCAA  404

Qy    121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
               |||||||||||||:::|||||||||||||||
Db    405  GAGTTCTTGGTGTAATGAACACCGAGTGGATAATAGAAAGT  446
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;   Sequence 1236, Application US/09023655
;   Patent No. 6607879
;   GENERAL INFORMATION:
;   APPLICANT: Cocks, Benjamin G.
;   APPLICANT: Susan G. Stuart
;   APPLICANT: Jeffrey J. Seilhamer
;   TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;   TITLE OF INVENTION: EXPRESSION
;   NUMBER OF SEQUENCES: 1508
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/023,655
;   FILING DATE: HEREWITH
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Zeller, Karen J.
;   REGISTRATION NUMBER: 37,071
;   REFERENCE/DOCKET NUMBER: PA-0001 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1236:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 816 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
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CLONE: g288309
US-09-023-655-1236

Alignment Scores:
Pred. No.:
Score:

Pred. No.:	1.41e-52	Length:	816
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Percent Similarity:	76.87%	Conservative:	17
Best Local Similarity:	64.18%	Mismatches:	31
Query Match:	60.92%	Indels:	0
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US-10-787-382-5 (1-134) x US-09-023-655-1236 (1-816)

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Qy    21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThrHis         40
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Qy    41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
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Db   165 CGAACTCTCGTCATTGGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAAATCAC  224

Qy    61 GlnLeuCysIleLysGluValPheGlnGlyTyrIleAspThrLeuLysAsnGlnThrAlaHis   80
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Db   225 CAACTGTGCACTGAAGAAAATCTTTCAGGGAATAGGCACACTGGACAGTCAAAACTGTGCAA  284

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Db   285 GGGGGGTACTGTGGGAAAGACTATTGAAAAACTTGTCCTTAATAAAGAAATACAATTGACGGC  344

Qy   101 GlnIleLysArgCysAlaGlyGlyArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
           |||||||           :::||||||||||||||||||||||||||
Db   345 CAAAAAAAAAAGTGTGGAAGAGAAAGACCGGAGTAAACCAAATTCCTAGACTACCTGCAA  404

Qy   121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
           |||||||::::|||::::|||||||                 |||||
Db   405 GAGTTTCTTGGTGTTAATGAACACCCAGTGGATAAATAGAAAGT  446
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Search completed: August 7, 2005, 00:14:16
Job time : 121.932 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 6, 2005, 22:43:11 ; Search time 556.45 Seconds
                                           (without alignments)
                                           1561.024 Million cell updates/sec

               Copyright (c) 1993 - 2005 Compugen Ltd.
               GenCore version 5.1.6

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLINLSLLALGAAYVSAF..........FLDYLQVFLGVINTEWTPES 134

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Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10787382 @CGN_1_1_879 @runat_04082005_084754_19405
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
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SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	696	100.0	402	9	US-09-755-633-7	Sequence 7, Appli
2	696	100.0	402	9	US-09-755-633-8	Sequence 8, Appli
3	696	100.0	402	14	US-10-218-654-83	Sequence 83, Appl
4	696	100.0	402	14	US-10-218-654-84	Sequence 84, Appl
5	696	100.0	402	15	US-10-262-439-83	Sequence 83, Appl
6	696	100.0	402	15	US-10-262-439-84	Sequence 84, Appl
7	696	100.0	402	19	US-10-787-382-7	Sequence 7, Appli
8	696	100.0	402	19	US-10-787-382-8	Sequence 8, Appli
9	696	100.0	402	9	US-09-755-633-4	Sequence 4, Appli
10	696	100.0	402	9	US-09-755-633-6	Sequence 6, Appli
11	696	100.0	610	14	US-10-218-654-80	Sequence 80, Appl
12	696	100.0	610	14	US-10-218-654-82	Sequence 82, Appl
13	696	100.0	610	15	US-10-262-439-80	Sequence 80, Appl
14	696	100.0	610	15	US-10-262-439-82	Sequence 82, Appl
15	696	100.0	610	19	US-10-787-382-4	Sequence 4, Appli
16	696	100.0	610	19	US-10-787-382-6	Sequence 6, Appli
17	632.5	100.0	671	19	US-10-787-382-21	Sequence 21, Appl
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20	610	87.6	345	14	US-10-218-654-85	Sequence 85, Appl
21	610	87.6	345	17	US-10-191-997-90	Sequence 90, Appl
22	610	87.6	345	15	US-10-262-439-85	Sequence 85, Appl
23	610	87.6	345	15	US-10-262-439-87	Sequence 87, Appl
24	610	87.6	345	19	US-10-787-382-9	Sequence 9, Appli
25	610	87.6	345	15	US-10-262-439-87	Sequence 87, Appl
26	610	87.6	459	20	US-10-787-382-19	Sequence 11, Appl
27	610	87.6	459	22	US-10-787-382-11	Sequence 11, Appl
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29	430	61.8	816	21	US-10-191-997-90	Sequence 4, Appli
30	430	61.8	816	22	US-10-880-101A-87	Sequence 87, Appl
31	430	61.8	858	16	US-10-295-074-8	Sequence 8, Appli
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33	430	61.8	858	20	US-10-846-911-8	Sequence 8, Appli
34	430	61.8	858	20	US-10-846-911-10	Sequence 10, Appl
35	428	61.5	1658	9	US-09-755-633-19	Sequence 19, Appl
36	428	61.5	1658	18	US-10-787-382-19	Sequence 19, Appl
37	424	60.9	816	18	US-10-641-643-1236	Sequence 1236, Ap
38	424	60.9	864	16	US-10-295-074-14	Sequence 14, Appl
39	415.5	59.7	864	16	US-10-846-911-14	Sequence 14, Appl
40	413.5	59.4	864	20	US-10-295-074-12	Sequence 12, Appl
41	413.5	59.4	864	20	US-10-846-911-12	Sequence 12, Appl
42	406.5	58.4	1658	19	US-09-755-633-18	Sequence 18, Appl
43	406.5	58.4	1658	22	US-10-787-382-18	Sequence 18, Appl
44	228.5	32.8	3241	22	US-10-880-101A-91	Sequence 91, Appl
45	222	31.9	6727	9	US-09-800-629A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-755-633-7
Sequence 7, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306

Pred. No. is the number of results predicted by chance to have a

; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-755-633-7

Alignment Scores:

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Pred. No.:
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Percent Similarity:       100.00%       Matches:       134
Best Local Similarity:    100.00%       Conservative:    0
Query Match:              9             Mismatches:      0
DB:                                     Indels:          0
                                        Gaps:            0
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US-10-787-382-5 (1-134) x US-09-755-633-7 (1-402)

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Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Db  361  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 402
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RESULT 2
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; Sequence 8, Application US/0975633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-755-633-8

Alignment Scores:

; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
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;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-218-654-83

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Query Match:              9             Mismatches:      0
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US-10-787-382-5 (1-134) x US-09-755-633-8 (1-402)

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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuValAlaLeuGlyAlaAlaThrTyrValSerAlaAlaPhe 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCCTCTCTGGGGGCTGCCTCATGTTTCTGCCTTT 343

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  222  CAACTGTGCATTAAAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCCAC 163

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  282  CGAACTTGGCTGATAGGCGATGGGGAACCTGACCTCTACTCCTGAAAATAAAATCAC 223

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuAsnGlnThrAlaHis 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  222  GCTGTGAAAAATCCCATGAATAGACTGGTGGCAGAGAACCTTGACACTGCTTCCACTCAT 283

Qy   81  GlyGluValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  162  GGGGAGGCTGTGGATAAATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC 103

Qy  101  GlnLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  102  CAAAAAAAGTGTTGCAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 43

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
         ||||||||||||||||||||||||||||||||||||
Db   42  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1
```

RESULT 3
US-10-218-654-83
; Sequence 83, Application US/10218654
; Publication No. US2003099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-218-654-83

Alignment Scores:

```
Pred. No.:
Score:                    5.48e-89      Length:        402
Percent Similarity:       100.00%       Matches:       134
Best Local Similarity:    100.00%       Conservative:    0
Query Match:              14            Mismatches:      0
DB:                                     Indels:          0
                                        Gaps:            0
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US-10-787-382-5 (1-134) x US-10-218-654-83 (1-402)

RESULT 4
US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Alignment Scores:
Pred. No.:
Score: 5.48e-89   Length: 402
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 14   Mismatches: 0
DB: Indels: 0
                  Gaps: 0

US-10-787-382-5 (1-134) x US-10-218-654-84 (1-402)

```
Qy    1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
Db    1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGGTTTCTGCCTTT  60

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis     40
Db   61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGACTCTCTCCACTCAT     120

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
Db  121 CGAACTGGCTGATAGGCGATGGGAACCCTGATGATTCCTACTCCTGAAAAATAAAAATCAC 180

Qy   61 GlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHis 80
Db  181 CAACTGTGCATTAAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCCAC  240

Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
Db  241 GGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAGAGAACACATTAGAGCGC 300

Qy  101 GlnLeuLysArgCysAlaGlyGlyAsnLeuAspTyrLeuGln                    120
Db  301 CAAAAAAAAGGTGTCCAGGAGAAGATGGAGAGTTCCTAGACTACTACCTGCAA        360

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                   134
Db  361 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT                    402
```

RESULT 5
US-10-262-439-83
; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83

Alignment Scores:
Pred. No.:
Score: 5.48e-89   Length: 402
Percent Similarity: 100.00%   Matches: 134
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 15   Mismatches: 0
DB: Indels: 0
                  Gaps: 0

US-10-787-382-5 (1-134) x US-10-262-439-83 (1-402)

```
Qy    1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
Db    1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGGTTTCTGCCTTT  60

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis     40
Db   61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGACTCTCTCCACTCAT     120

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
Db  121 CGAACTTGGCTGATAGGCGATGGGAACCCTGATGATTCCTACTCCTATTGAAGAACCAAAACTGCCAC 180

Qy   61 GlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHis 80
Db  222 CAACTGTGCATTAAAAGAAGTTGTGCAGGGGAGAAGATGGAGAGTTCCTAGACTACTACCTGCAA 163
Db  282 CGAACCTTGGGCTGCCTATAGGCGATGGGAACCCTGATGATTCCTACTCCTTAGAAAAATCAC 223

Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
Db  162 GGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATTAGAGCGC 103

Qy  101 GlnLeuLysArgCysAlaGlyGlyAsnLeuAspTyrLeuGln                    120
Db  102 CGAACTTGGCTGATAGGCGATGGGAACCCTGATGATTCCTACTCCTATTGAAGAACCAAAACTGCCAC 43

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer                   134
Db   42 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT                      1
```

```
Qy      81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300

Qy     101 GlnLysLysArgCysAlaGlyAlaGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CAAAAAAAAGGTGTGCAGGAGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360

Qy     121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
           |||||||||||||||||||||||||||||||||||
Db     361 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT 402
```

RESULT 6
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLBIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84

Alignment Scores:
Pred. No.:
Score: 5.4e-89
Percent Similarity: 696.00
Best Local Similarity: 100.00%
Query Match: 100.00%
                            15

Length: 402
Matches: 134
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-787-382-5 (1-134) x US-10-262-439-84 (1-402)

```
Qy       1 MetArgMetLeuLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGCCTATGTTTCTGCCTTT 343

Qy      21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTGACACTGCTCCACTCAT 283

Qy      41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     342 CGAACTTGGCTGATAGGCGATGGGAACCTGATGAATCCTACTCCTGAAAATAAAAATCAC 223

Qy      61 GlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHis 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     222 CAACTGTGCATAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 163

Qy      81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     162 GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAGCGC 103

Qy     101 GlnLysLysArgCysAlaGlyAlaGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     102 CAAAAAAAAGGTGTGCAGGAGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 43
```

RESULT 7
US-10-787-382-7
; Sequence 7, Application US/10787382
; Publication No. US2004019I868A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; APPLICANT: Yang, Shumin
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLBIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-787-382-7

Alignment Scores:
Pred. No.:
Score: 5.4e-89
Percent Similarity: 696.00
Best Local Similarity: 100.00%
Query Match: 100.00%
                            19

Length: 402
Matches: 134
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-787-382-5 (1-134) x US-10-787-382-7 (1-402)

```
Qy       1 MetArgMetLeuLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGCCTATGTTTCTGCCTTT 180

Qy      41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGAATCCTACTCCTGAAAATAAAAATCAC 180

Qy      21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTGACACTGCTCCACTCAT 120

Qy      61 GlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHis 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CAACTGTGCATAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240

Qy      81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300

Qy     101 GlnLysLysArgCysAlaGlyAlaGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAAAAAAAAGGTGTGCAGGAGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360

Qy     121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
           |||||||||||||||||||||||||||||||||||
Db     361 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT 402
```

RESULT 8
US-10-787-382-8/c
; Sequence 8, Application US/10787382
```
Qy     121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
           |||||||||||||||||||||||||||||||||||
Db      42 GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT 1
```

Publication No. US20040191868A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/10/787,382
CURRENT FILING DATE: 2004-02-24
PRIOR APPLICATION NUMBER: US/09/755,633
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-10-787-382-8

Alignment Scores:
Pred. No.:
Score: 5.48e-89
Percent Similarity: 100.00%   Length: 402
Best Local Similarity: 100.00%   Matches: 134
Query Match: 100.00%   Conservative: 0
DB: 19   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

US-10-787-382-5 (1-134) x US-10-787-382-8 (1-402)

```
Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  402  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 343

Qy   21  AlaValAlaGlnAsnProMetAsnArgLeuValAlaLeuGlyThrLeuThrLeuSerThrHis  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  342  GCTGTAGAAAATCCCATGAATAGACTCGGTGGCGAGAGACCTTGACACTGTCCTCCACTCAT 283

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  282  CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 223

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysGlnThrAlaHis  80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  222  CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCCAC 163

Qy   81  GlyGluValAspLysPheLeuAsnLeuSerLeuIleLysGluHisIleIleGluArg  100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  162  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC 103

Qy  101  GlnLysGlyArgCysAlaGlyLeuGluArgTrpAspTyrLeuGln  120
            |||||||||||||||||||||||||||||||||||||||||||||
Db  102  CAAAAAAAAGGTGTCCAGGAGAGATGGGACAGTTCCTAGACTACCTGCAA 43

Qy  121  ValPheLeuGlyValIleLeuAsnThrGluTrpProGluSer 134
            ||||||||||||||||||||||||||||||||||||||||||
Db   42  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT 1
```

RESULT 9
US-09-755-633-4
Sequence 4, Application US/0975633
Patent No. US20020127200A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(430)
US-09-755-633-4

Alignment Scores:
Pred. No.:
Score: 1.03e-88
Percent Similarity: 100.00%   Length: 610
Best Local Similarity: 100.00%   Matches: 134
Query Match: 100.00%   Conservative: 0
DB: 9   Mismatches: 0
                                       Indels: 0
                                       Gaps: 0

US-10-787-382-5 (1-134) x US-09-755-633-4 (1-610)

```
Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 88

Qy   21  AlaValAlaGlnAsnProMetAsnArgLeuValAlaLeuGlyThrLeuThrLeuSerThrHis  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89  GCTGTAGAAAATCCCATGAATAGACTCGGTGGCGAGAGACCTTGACACTGTCCTCCACTCAT 148

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149  CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC 208

Qy   61  GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysGlnThrAlaHis  80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209  CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCCAC 268

Qy   81  GlyGluValAspLysPheLeuAsnLeuSerLeuIleLysGluHisIleIleGluArg  100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  269  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC 328

Qy  101  GlnLysGlyArgCysAlaGlyLeuGluArgTrpAspTyrLeuGln  120
            |||||||||||||||||||||||||||||||||||||||||||||
Db  329  CAAAAAAAAGGTGTCCAGGAGAGATGGGACAGTTCCTAGACTACCTGCAA 388

Qy  121  ValPheLeuGlyValIleLeuAsnThrGluTrpProGluSer 134
            ||||||||||||||||||||||||||||||||||||||||||
Db  389  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT 430
```

RESULT 10
US-09-755-633-6/c
Sequence 6, Application US/09755633
Patent No. US20020127200A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21

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SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Alignment Scores:
Pred. No.:
Score:                     1.03e-88        Length:       610
Percent Similarity:        696.00          Matches:      134
Best Local Similarity:     100.00%         Conservative: 0
Query Match:               100.00%         Mismatches:   0
DB:                        9               Indels:       0
                                           Gaps:         0
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US-10-787-382-5 (1-134) x US-09-755-633-6 (1-610)

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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuLeuGlyAlaAlaLeuTyrValSerAlaPhe   20
Db  582  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGGCTGCCTATGTTTCTGCCTTT  523

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis   40
Db  522  GCTGTAGAAAATCCCATGAATAGACTGGTGGCCAGAGACCTTGACACTGCTCTCCACTCAT  463

Qy   41  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
Db  462  CGAACTTGGCTGATAGGGTACGATGGAAACCTGATGATTCCTACTCCTGAAAATAAAATCAC  403

Qy   61  GlnLeuCysIleLeuLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis  80
Db  402  CAACTGTGCATTAAGGAAGTTTTTCAGGGTATAGACACAATTGAAGAACCAAAACTGCCCAC  343

Qy   81  GlyGluValAlaAspLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
Db  342  GGGGAGGTGGCTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC  283

Qy  101  GlnLeuLysArgCysAlaGlyValThrArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
Db  282  CAAAAAAAGGTGTGCAGGAGAAAGATGGACAGAGTTCCTAGACTACCTGCAA  223

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
Db  222  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT  181
```

```
Alignment Scores:
Pred. No.:
Score:                     1.03e-88        Length:       610
Percent Similarity:        696.00          Matches:      134
Best Local Similarity:     100.00%         Conservative: 0
Query Match:               100.00%         Mismatches:   0
US-10-218-654-82           14              Indels:       0
DB:                                        Gaps:         0
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US-10-787-382-5 (1-134) x US-10-218-654-80 (1-610)

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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuLeuGlyAlaAlaLeuTyrValSerAlaPhe   20
Db   29  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGGCTGCCTTATGTTTCTGCCTTT  88

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis   40
Db   89  GCTGTAGAAAATCCCATGAATAGACTGGTGGCCAGAGACCTTGACACTGCTCTCCACTCAT  148

Qy   41  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
Db  149  CGAACTTGGCTGATAGGGTACGATGGAAACCTGATGATTCCTACTCCTGAAAATAAAATCAC  208

Qy   61  GlnLeuCysIleLeuLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis  80
Db  209  CAACTGTGCATTAAGGAAGTTTTTCAGGGTATAGACACAATTGAAGAACCAAAACTGCCCAC  268

Qy   81  GlyGluValAlaAspLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg  100
Db  269  GGGGAGGTGGCTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC  328

Qy  101  GlnLeuLysArgCysAlaGlyValThrArgTrpArgValThrLysPheLeuAspTyrLeuGln  120
Db  329  CAAAAAAAGGTGTGCCAGGAGAAAGATGGAGAGAGTGACAAAGTTCCTAGACTACCTGCAA  388

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  134
Db  389  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT  430
```

```
Alignment Scores:
Pred. No.:
Score:                     1.03e-88        Length:       610
Percent Similarity:        696.00          Matches:      134
Best Local Similarity:     100.00%         Conservative: 0
Query Match:               100.00%         Mismatches:   0
US-10-218-654-82           14              Indels:       0
DB:                                        Gaps:         0
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US-10-787-382-5 (1-134) x US-10-218-654-82 (1-610)

Qy        1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe  20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      582 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGTGCCTATGTTTCTGCCTTT 523

Qy       21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTTGACACTGCTCTCCACTCAT 463

Qy       41 ArgThrTrpLeuIleLeuGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      462 CGAACTTGGCTGATAGGCGATGGGGAACCTGATGATTCCTACTCCTGAAAAATAAACAC 403

Qy       61 GlnLeuCysIleLysGlyLeuPheGlnGlyIleLeuAspThrLeuLysGlyValHisAlaHis  80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      402 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACATTGAAAGAGACCAAAGGTGCCCAC 343

Qy       81 GlyGluValAlaAspLysGlyLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      342 GGGGAGGTCGTGGATAAAGTTCCAAAACTTGTCTTTAATAAAAAGAACACATAGAGGC 283

Qy      101 GlnLeuGlyValAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      282 CAAAAAAAAGGTGTGCAGGAGAAGATGACAAAGTTCCTAGACTACCTGCA 223

Qy      121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
            ||||||||||||||||||||||||||||||||||||||||||
Db      222 GTATTTCTTGGGTGTAATAAACACCGAGTGGGACACCGAAAGT 181
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RESULT 13
US-10-262-439-80

; Sequence 80, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Dreitz, Matthew J.
;   APPLICANT: Wonderling, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C2
;   CURRENT APPLICATION NUMBER: US/10/262,439
;   CURRENT FILING DATE: 2002-09-30
;   PRIOR APPLICATION NUMBER: US/09/451,527
;   PRIOR FILING DATE: 1999-12-01
;   PRIOR APPLICATION NUMBER: 09/322,409
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 60/087,306
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 80
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(430)
US-10-262-439-80

  Alignment Scores:
  Pred. No.:
  Score:                 1.03e-88         Length:        610
  Percent Similarity:    696.00           Matches:       134
  Best Local Similarity: 100.00%          Conservative:  0
  Query Match:           100.00%          Mismatches:    0
  DB:                    15               Indels:        0
                                          Gaps:          0

US-10-787-382-5 (1-134) x US-10-262-439-80 (1-610)

Qy        1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe  20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      582 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGTGCCTATGTTTCTGCCTTT 523
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Db       29 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGTGCCTATGTTTCTGCCTTT  88

Qy       21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTTGACACTGCTCTCCACTCAT 148

Qy       41 ArgThrTrpLeuIleLeuGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      149 CGAACTTGGCTGATAGGCGATGGGGAACCTGATGATTCCTACTCCTGAAAAATAAACAC 208

Qy       61 GlnLeuCysIleLysGlyLeuPheGlnGlyIleLeuAspThrLeuLysGlyValHisAlaHis  80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      209 CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACATTGAAAGAGACCAAAGGTGCCCAC 268

Qy       81 GlyGluValAlaAspLysGlyLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      269 GGGGAGGTCGTGGATAAAGTTCCAAAACTTGTCTTTAATAAAAAGAACACATAGAGGC 328

Qy      101 GlnLeuGlyValAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      329 CAAAAAAAAGGTGTGCAGGAGAAGATGACAAAGTTCCTAGACTACCTGCA 388

Qy      121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
            ||||||||||||||||||||||||||||||||||||||||||
Db      389 GTATTTCTTGGGTGTAATAAACACCGAGTGGGACACCGAAAGT 430
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RESULT 14
US-10-262-439-82/c

; Sequence 82, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Dreitz, Matthew J.
;   APPLICANT: Wonderling, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C2
;   CURRENT APPLICATION NUMBER: US/10/262,439
;   CURRENT FILING DATE: 2002-09-30
;   PRIOR APPLICATION NUMBER: US/09/451,527
;   PRIOR FILING DATE: 1999-12-01
;   PRIOR APPLICATION NUMBER: 09/322,409
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 60/087,306
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-262-439-82

  Alignment Scores:
  Pred. No.:
  Score:                 1.03e-88         Length:        610
  Percent Similarity:    696.00           Matches:       134
  Best Local Similarity: 100.00%          Conservative:  0
  Query Match:           100.00%          Mismatches:    0
  DB:                    15               Indels:        0
                                          Gaps:          0

US-10-787-382-5 (1-134) x US-10-262-439-82 (1-610)

Qy        1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe  20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      582 ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCGTGCCTATGTTTCTGCCTTT 523

Qy       21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTTGACACTGCTCTCCACTCAT 463

Qy       41 ArgThrTrpLeuIleLeuGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
```

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Db   462  CGAACTTGGCTGATAGGCGATGGGAGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   402  CAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAAGAACCAAAACTGCCCAC  343

Qy    61  GlnLeuCysIleLysGlyValPheGlnGlyIleAspThrLeuLysGluHisIleGluArg
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81  GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg  100

Db   342  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC  283

Qy   101  GlnLysLysArgCysAlaGlyAlaGlyLeuArgTrpArgValThrLysSerPheLeuAspThrLeuGln  120
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   282  CAAAAAAAAAGGTGTGCAGGAGAAAGAATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA  223

Qy   121  ValPheLeuGlyValIleAsnThrGluTrpProGluSer  134
          |||||||||||||||||||||||
Db   222  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGGAAAGT  181
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RESULT 15
US-10-787-382-4

; Sequence 4, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 4
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(430)
US-10-787-382-4

Alignment Scores:
Pred. No.:
Score: 1.03e-88
Percent Similarity: 696.00   Length: 610
Best Local Similarity: 100.00%   Matches: 134
Query Match: 100.00%   Conservative: 0
DB: 100.00%   Mismatches: 0
                          19   Indels: 0
                                          Gaps: 0

US-10-787-382-5 (1-134) x US-10-787-382-4 (1-610)

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Qy     1  MetArgMetLeuLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe  20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGAGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT  88

Qy    21  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis  40
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    89  GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACTCAT  148

Qy    41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  60
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   149  CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAATCAC  208

Qy    61  GlnLeuCysIleLysGlyValPheGlnGlyIleAspThrLeuLysGluHisIleGluArg  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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(right column)

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Db   209  CAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAAGAACCAAAACTGCCCAC  268

Qy    81  GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   269  GGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAGCGC  328

Qy   101  GlnLysLysArgCysAlaGlyAlaGlyLeuArgTrpArgValThrLysSerPheLeuAspThrLeuGln  120
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   329  CAAAAAAAAAGGTGTGCAGGAGAAAGAATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA  388

Qy   121  ValPheLeuGlyValIleAsnThrGluTrpProGluSer  134
          |||||||||||||||||||||||
Db   389  GTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGGAAAGT  430
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Search completed: August 7, 2005, 03:15:59
Job time : 559.45 secs

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OM protein - nucleic search, using frame_plus_p2n model

                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:          August  6, 2005, 19:45:30 ; Search time 2814 Seconds
                                                (without alignments)
                                                1812.584 Million cell updates/sec

Title:           US-10-787-382-5
Perfect score:   696
Sequence:        1 MRMLLNLSLLALGAAYVSAF..........FLDYLQVFLGVINTEWTPES 134

Scoring table:   BLOSUM62
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                 Ygapop   10.0 ; Ygapext   0.5
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                 Delop     6.0 ; Delext    7.0

Searched:        34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:     68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       EST:*
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                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                    SUMMARIES
                               #
Result            Query
No.  Score  Match  Length  DB  ID          Description
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   1  430   61.8    405    9   AY412020    AY412020 Homo sapi
   2  430   61.8    405    9   CD559532    CD559532 AGENCOURT
c  3  430   61.8    456    6   CD559686    CD559686 AGENCOURT
c  4  430   61.8    470    6   CD559687    CD559687 AGENCOURT
c  5  430   61.8    492    6   CD559533    CD559533 AGENCOURT
c  6  430   59.9    458    3   BC062279    BC062279 Homo sapi
   7  417   59.9    458    9   BC066280    BC066280 Homo sapi
c  8  417   59.9    463    6   CD559535    CD559535 AGENCOURT
c  9  417   59.9    467    6   CD559690    CD559690 AGENCOURT
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   11   417   59.9   489   6   CD559536   CD559536 AGENCOURT
   12   417   59.9   817   3   BC069137   BC069137 Homo sapi
   13   417   59.1   405   9   AY412021   AY412021 Pan trogl
   14   406   58.3   456   3   BC066281   BC066281 Homo sapi
c  15   406   58.3   467   6   CD559688   CD559688 AGENCOURT
   16   406   58.3   478   6   CD559534   CD559534 AGENCOURT
   17   383   55.0   477   6   CD559608   CD559608 AGENCOURT
   18   336   51.2   622   9   CE331159   CE331159 tigr-gss-
   19   336   48.3   399   9   AY412022   AY412022 Mus muscu
   20   186   26.7   781   9   CR235404   CR235404 Reverse s
c  21   165   23.7   503   5   BQ598873   BQ598873 MI-B-E4-a
c  22   129   18.5   495   7   CR554944   CR554944 DKFzp469N
c  23   94.5  13.6   737   9   CR026247   CR026247 Reverse s
c  24   91.5  13.1   811   4   BI247887   BI247887 602259820
c  25   88.5  12.7   681   5   CD894793   CD894793 G118.127C
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c  27   84    12.1   496   1   AA689677   AA689677 v80C02.r
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c  29   81.5  11.7   703   9   CI301640   CI301640 gbs2_CH25
c  30   81.5  11.7   769   5   BU227588   BU227588 603800631
c  31   81.5  11.7   772   7   CF234700   CF234700 PtaJXT001
c  32   81    11.6   1267  3   CR727373   CR727373 Tetraodon
c  33   80.5  11.6   518   4   BM284184   BM284184 k13b02.y
c  34   80.5  11.6   589   5   CD305286   CD305286 StrPu691.
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c  37   79.5  11.4   675   4   BI561257   BI561257 603256408
c  38   79    11.4   425   2   AW068198   AW068198 cn23c07.y
c  39   79    11.4   504   6   CB047608   CB047608 NISC_gg03
c  40   79    11.4   560   1   AJ745225   AJ745225 BovGen 24
c  41   79    11.4   607   5   CO896018   CO896018 UI-H-DHI-
c  42   79    11.4   644   5   BQ018244   BQ018244 UI-H-DHI-
c  43   79    11.4   644   6   CB047607   CB047607 NISC_gg03
c  44   79    11.4   660   7   CN371286   CN371286 17006/000
c  45   79    11.4   666   6   CA311187   CA311187 UI-CP-FN0
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                                    ALIGNMENTS

RESULT 1
LOCUS       AY412020                405 bp    DNA     linear    GSS 16-DEC-2003
DEFINITION  Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION   AY412020
VERSION     AY412020.1  GI:39767985
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 405)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..405
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Column 1

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                    gene            /organism="Homo sapiens"
                                    /mol_type="genomic DNA"
                                    /db_xref="taxon:9606"
                                    /gene="IL5"
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                                    /locus_tag="HCM4418"

ORIGIN

Alignment Scores:
Pred. No.:                          1.43e-44
Score:                              430.00         Length:         405
Percent Similarity:                 77.61%         Matches:        87
Best Local Similarity:              64.93%         Conservative:   17
Query Match:                        61.78%         Mismatches:     30
DB:                                 9              Indels:         0
                                                   Gaps:           0

US-10-787-382-5 (1-134) x AY412020 (1-405)

Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe   20
         |||||||||||| ::||||||||||||||||||||||||||||||| |||
Db    1  ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCACGTGTATGGCCATC   60

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaLeuGluThrLeuThrLeuLeuSerThrHis   40
         ||| :::|||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CCCACAGAAATTCCCACAAGTGCCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT   120

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
         |||          ::|   |||||||||||||||||||||||||||||||||||||||
Db  121  CGAACTCTGCATGGTGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAATCAC   180

Qy   61  GlnLeuCysIleLeuLysGlyLeuValPheGlnGlyIleLeuAspTyrLeuLysAsnGlnThrAlaHis   80
         ||||||||| ::||||||||||||||||||||:::||||||||||||||||||||||||
Db  181  CAACACTGTCACTGAGAAGAAATCTTTCAGGGAATAGGCCACACTGGAGAGTCAAACTGTGCAA   240

Qy   81  GlyGluAlaValAspLysLysPheGlnAsnLeuSerLeuIleLeuLysGluHisIleLleGluArg   100
         |||||| :::||||||||||||||||||||||::::||||||::::|||||::
Db  241  GGGGGGTACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGACGGC   300

Qy  101  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
         :::|||||||||||||||||||||||||||||||||
Db  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
         ||||| |||||||||||||||||||||||||||||||||||
Db  361  GAGTTTCTTGGTGTAATGAACACCGAGTGGATAATAGAAAGT   402
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Column 2 (us-10-787-382-5.rst)

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FEATURES             Location/Qualifiers
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                     High quality sequence stop:456.
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971772"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual;
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."
```

```
ORIGIN

http://image.llnl.gov
Plate: IRBK1 row: g  column: 11
High quality sequence stop: 456.

Alignment Scores:
Pred. No.:                          1.69e-44
Score:                              430.00         Length:         456
Percent Similarity:                 77.61%         Matches:        87
Best Local Similarity:              64.93%         Conservative:   17
Query Match:                        61.78%         Mismatches:     30
DB:                                 6              Indels:         0
                                                   Gaps:           0

US-10-787-382-5 (1-134) x CD559532 (1-456)

Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe   20
         |||||||||||| ::||||||||||||||||||||||||||||||| |||
Db   22  ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCACGTGTATGGCCATC   81

Qy   21  AlaValGluAsnProMetAsnArgLeuValAlaLeuGluThrLeuThrLeuLeuSerThrHis   40
         ||| :::|||||||||||||||||||||||||||||||||||||||||||||||||
Db   82  CCCACAGAAATTCCCACAAGTGCCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT   141

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
         |||          ::|   |||||||||||||||||||||||||||||||||||||||
Db  142  CGAACTCTGCATGGTGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAATCAC   201

Qy   61  GlnLeuCysIleLeuLysGlyLeuValPheGlnGlyIleLeuAspTyrLeuLysAsnGlnThrAlaHis   80
         ||||||||| ::||||||||||||||||||||:::||||||||||||||||||||||||
Db  202  CAACACTGTCACTGAGAAGAAATCTTTCAGGGAATAGGCCACACTGGAGAGTCAAACTGTGCAA   261

Qy   81  GlyGluAlaValAspLysLysPheGlnAsnLeuSerLeuIleLeuLysGluHisIleLleGluArg   100
         |||||| :::||||||||||||||||||||||::::||||||::::|||||::
Db  262  GGGGGGTACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGACGGC   321

Qy  101  GlnLeuLysLysAlaArgCysAlaLysGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln   120
         |||:::||| :::|||||||||||:::||||||||||||||||||||||||||||
Db  322  CAAAAAAAAAGTGTGGAGAAGAAAGACGGAGAGTAAAACCAATTCCTAGAGACTACCTGCAA   381

Qy  121  ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer   134
         ||||| |||||||||||||||||||||||||||||||||||
Db  382  GAGTTTCTTGGTGTAATGAACACCGAGTGGATAATAGAAAGT   423
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RESULT 3

ACCESSION IMAGE:6971772 3', mRNA sequence.
VERSION CD559686
 CD559686.1 GI:31585754
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT National Cancer Institute / NIH
 Office of Cancer Genomics
 Contact: Daniela S. Gerhard, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: g column: 11
 High quality sequence stop: 456.
FEATURES Location/Qualifiers
 source 1..456
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:6971772"
  /tissue_type="mixed"
  /lab_host="DH5A (T1 phage-resistant)"
  /clone_lib="NIH_MGC_195"
  /note="Vector: pDNR-Dual; Site 1: loxP-SalI; Site 2:
  loxP-HindIII; Clones from this library have been
  PCR-amplified using gene-specific primers to contain the
  complete open reading frame (based on known gene sequences
  available from NCBI's RefSeq). Template for PCR is cDNA
  derived from either pooled cytoplasmic polyA RNA from 30
  cells lines or pooled total RNA from 10 different tissues
  (from BD Biosciences/Clontech and Washington University).
  PCR products are directionally cloned into the loxP sites
  of the pDNR-Dual vector. Library constructed by Dr.
  Narayan Bhat, Earl Bere III and Hongling Liao (Gene
  Expression Laboratory, Research Technology Program, SAIC
  Frederick, NCI-Frederick, Frederick, MD 21702). For
  information on which gene each clone represents, please
  visit our anonymous ftp site at
  ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presV.dat
  a Note: this is a NIH_MGC Library."

ORIGIN

US-10-787-382-5 (1-134) x CD559686 (1-456)

Alignment Scores:
Pred. No.:
Score: 1.69e-44
  430.00
Percent Similarity: 77.61%
Best Local Similarity: 64.93%
Query Match: 61.78%
DB: 6

Length: 456
Matches: 87
Conservative: 17
Mismatches: 30
Indels: 0
Gaps: 0

Qy 1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
 ||||||||||||||||||||||||||||||||||||||||:::||||||::::|||
Db 433 ATGAGGATGCTTCTGAACCTTTGAGTTTGCTRAGCTCTTGGAGCTGCCTRACGTGTAATGGCCATC 374
Qy 21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
 ||| ||||| ::: |||||||||||||||||||||||||
Db 373 CCCACAGAGAATTCCACAAGTGCATTGGTGAAAGAGACACCTTGGCACTGCTTTCTACTCAT 314
Qy 41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60

Db 313 CGAACTCGGCTGATAGCCAAATGAGACTCTGAGGATTCCTTGTTCCTGTGTACATAAAAATCAC 254
Qy 61 GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
 ||||||||||||||||||:::||||||||||||||:::||||||
Db 253 CAACTGTGCACTGAAGAAAGTCTTTCAGGGAATAGCCACACTGAGAGTCAAACTGTGCAA 194
Qy 81 GlyGluAlaValAspProLysLeuPheGlnAsnLeuSerLeuLeuAlaLeuGlyLysGluHisGluArg 100
 ||| |||||||||||||||||||||||||:::||:::||:::
Db 193 GGGGGTACTGTGGAAGACTAATTCAAAAACTTGTTCCTTAATAAGAAAATTACATTGACGGC 134
Qy 101 GlnLysArgCysSerAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
 ||||||:::||||||||||||||||||||||||
Db 133 CAAAAAAAAAAAACGTGGAAGAAGAAGACGGAGCGAGGTAAACCAATTCCTAGACTACCACCTGCAA 74
Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Db 73 GAGTTTCTTGGTTGTAATGAACACCGAGTGGTATAATAGAAAGT 32

RESULT 4
CD559687/c
LOCUS CD559687 470 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14497029 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971771 5', mRNA sequence.
ACCESSION CD559687
VERSION CD559687.2 GI:38453484
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 470)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585755.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: g column: 10
 High quality sequence start: 14
 High quality sequence stop: 470.
FEATURES Location/Qualifiers
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  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:6971771"
  /tissue_type="mixed"
  /lab_host="DH5A (T1 phage-resistant)"
  /clone_lib="NIH_MGC_195"
  /note="Vector: pDNR-Dual; Site 1: loxP-SalI; Site 2:
  loxP-HindIII; Clones from this library have been
  PCR-amplified using gene-specific primers to contain the
  complete open reading frame (based on known gene sequences
  available from NCBI's RefSeq). Template for PCR is cDNA
  derived from either pooled cytoplasmic polyA RNA from 30
  cells lines or pooled total RNA from 10 different tissues
  (from BD Biosciences/Clontech and Washington University).
  PCR products are directionally cloned into the loxP sites
  of the pDNR-Dual vector. Library constructed by Dr.
  Narayan Bhat, Earl Bere III and Hongling Liao (Gene
  Expression Laboratory, Research Technology Program, SAIC
  Frederick, NCI-Frederick, Frederick, MD 21702). For

ORIGIN
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

Alignment Scores:
Pred. No.:   1.76e-44   Length: 470
Score: 430.00   Matches: 87
Percent Similarity: 77.61%   Conservative: 17
Best Local Similarity: 64.93%   Mismatches: 30
Query Match: 61.78%   Indels: 0
DB: 6   Gaps: 0

US-10-787-382-5 (1-134) x CD559687 (1-470)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaLaThrValSerAlaPhe 20
          ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||| |||
Db 446 ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC 387

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
          ||| ::: ||||||||||||||||||||||||||||||||||| |||
Db 386 CCCACAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT 327

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
          ||||| ||| |||::: |||||| :::||||||||||||||
Db 326 CGAACTCTGCTGAATAGCCAATGACAGTCCTGAGGATTCCTGTTCCTGTACATAAAATCAC 267

Qy   61 GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
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Db 266 CAAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 207

Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 206 GGGGGTACTGTGGAAAAGACTATTCAAAAACTGTCCTTAATAAAGAAATACATTGACGGC 147

Qy 101 GlnLysGlyArgGlyCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
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Db 146 CAAAAAAAAAAGTGTGGAGAAAGACCGGAGAGTAAACCAAATTCCTAGACTACCTGCAA 87

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Db   86 GAGTTTCTTGGTGTAATGAACACCGACGTGGATAATAGAAAGT 45

RESULT 5
CD559533
LOCUS   CD559533   492 bp   mRNA   linear   EST 26-NOV-2003
DEFINITION   AGENCOURT 14496993 NIH_MGC_195 Homo sapiens cDNA clone
             IMAGE:6971771 5', mRNA sequence.
ACCESSION   CD559533
VERSION   CD559533.2   GI:38558947
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 492)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585601.
             Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov

FEATURES   Location/Qualifiers
     source   1..492
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971771"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.:   1.88e-44   Length: 492
Score: 430.00   Matches: 87
Percent Similarity: 77.61%   Conservative: 17
Best Local Similarity: 64.93%   Mismatches: 30
Query Match: 61.78%   Indels: 0
DB: 6   Gaps: 0

US-10-787-382-5 (1-134) x CD559533 (1-492)

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaLaThrValSerAlaPhe 20
          ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||| |||
Db   56 ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC 115

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
          ||| ::: ||||||||||||||||||||||||||||||||||| |||
Db 116 CCCACAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT 175

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
          ||||| ||| |||::: |||||| :::||||||||||||||
Db 176 CGAACTCTGCTGAATAGCCAATGACAGTCCTGAGGATTCCTGTTCCTGTACATAAAATCAC 235

Qy   61 GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
          |||||||||||||||:::|||||||||||||||||||||||:::||||||||||||||||
Db 236 CAAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 295

Qy   81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluHisIleGluArg 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 296 GGGGGTACTGTGGAAAAGACTATTCAAAAACTGTCCTTAATAAAGAAATACATTGACGGC 355

Qy 101 GlnLysGlyArgGlyCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 120
          ||||| |||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db 356 CAAAAAAAAAAGTGTGGAGAAAGACCGGAGAGTAAACCAAATTCCTAGACTACCTGCAA 415

Qy 121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
          |||||||:::|||||||||||||||||||||||||||| ||||||
Db 416 GAGTTTCTTGGTGTAATGAACACCGACGTGGATAATAGAAAGT 457

RESULT 6
BC066279
LOCUS   BC066279   458 bp   mRNA   linear   HTC 12-FEB-2004
DEFINITION   Homo sapiens cDNA clone IMAGE:6971768, containing frame-shift

ACCESSION   BC066279
VERSION   BC066279.1 GI:42490901
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 458)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
             Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
             Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
             Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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             Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
             Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
             Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
             Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
             Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
             Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
             Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE   2 (bases 1 to 458)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             DNA Sequencing by: Sequencing Group at the Stanford Human Genome
             Center, Stanford University School of Medicine, Stanford, CA 94305
             Web site: http://www-shgc.stanford.edu
             Contact: (Dickson, Mark) mcd@paxil.stanford.edu
             Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
             R. M.
             clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAK Plat: 172 Row: a Column: 15
             This clone was selected for full length sequencing because it
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             This clone has the following problem: frame shifted.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971768"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
ORIGIN
Alignment Scores:
Pred. No.:   1
Score: 417.00
Percent Similarity: 77.04%

<page break>

Best Local Similarity: 64.44%   Mismatches: 30
Query Match: 59.91%   Indels: 1
DB: 3   Gaps: 0

RESULT 7
BC066280
LOCUS   BC066280   458 bp   mRNA   linear   HTC 12-FEB-2004
DEFINITION Homo sapiens cDNA clone IMAGE:6971769, containing frame-shift
            errors.
ACCESSION   BC066280
VERSION   BC066280.1 GI:42490838
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 458)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE   2 (bases 1 to 458)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian

Qy   1 MetArgMetLeuLeuMetLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
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Db   24 ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCCTACGTGTATGCCATC 83

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluValThrLeuThrLeuLeuSerThrHis 40
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Db 324 CAAAAAAAAAGTGTGGAGAAGAAACCAATTCCTAGACTACCTCCA 383

Qy 120 nValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
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Db 384 AGAGTTTCTTCGTGTAATGAACACCGAGTGGATAAATGAAAAGT 426

Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Bhat Laboratory
                cDNA Library Preparation: Bhat Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Sequencing Group at the Stanford Human Genome
                Center, Stanford University School of Medicine, Stanford, CA 94305
                Web site: http://www-shgc.stanford.edu
                Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
                R. M.

FEATURES   source
                This clone has the following problem: frame shifted.
                passed the following selection criteria: matched mRNA gi: 28559032
                clone="IMAGE:6971769"
                This clone was selected for full length sequencing because it
                Series: IRAK Plate: 172 Row: a Column: 16
                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                Clone distribution: MGC clone distribution information can be found
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                /db_xref="taxon:9606"
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                Location/Qualifiers

ORIGIN

US-10-787-382-5 (1-134) x BC066280 (1-459)

Alignment Scores:
Pred. No.:
Score: 7.86e-43
Percent Similarity: 417.00   Length: 458
Best Local Similarity: 77.04%   Matches: 87
Query Match: 64.44%   Conservative: 17
                        59.91%   Mismatches: 30
                        3   Indels: 1
                                        Gaps: 0

  1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuLeuLeuValAlaLeuGlyAlaAlaThrTyrValSerAlaPhe 20
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 21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis 40
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 84 CCCACAGAAATCCCACAGTGCATTGGTAGAAAGACACCTTGGCACTGCTTCTACTCAT 143

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144 CGAACTCTGCTTGAATAGGCCAATGAGGACTTCCTGGTTCCTGTTACATAAAAATCAC 203

 61 GlnLeuCysHisLeuGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 80
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264 GGGGGCTACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGACGGC 323

101 GlnLysLysArgCysAlaGlyValArgTrpArgValThrLysLysPheLeuAspTyrLeuGlyI 120
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324 CAAAAAAAAAGTGTCGGAAGAAGACCGGAGTAAACCAATTCCTAGACTACACTGCA 383

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    ||||:::||||||:::|||
384 AGAGTTTCTTGGTGTAATGAACACGGAGTGGATAATAGAAAGT 426

, RESULT 8

CD559535
LOCUS   CD559535   463 bp   mRNA   linear   EST 26-NOV-2003
DEFINITION   AGENCOURT_14496865 NIH_MGC_195 Homo sapiens cDNA clone
                IMAGE:6971769 5', mRNA sequence.
ACCESSION   CD559535
VERSION   CD559535.2 GI:38558950
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
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                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 463)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585603.
                Contact: Daniela S. Gerhard, Ph.D.
                Office of Cancer Genomics
                National Cancer Institute / NIH
                Bldg. 31 Rm10A07 Bethesda, MD 20892
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Bhat Laboratory
                cDNA Library Preparation: Bhat Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: IRBK1 row: g column: 08
                High quality sequence stop: 463.

FEATURES   Location/Qualifiers
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                                PCR-amplified using gene-specific primers to contain the
                                complete open reading frame (based on known gene sequences
                                available from NCBI's RefSeq). Template for PCR is cDNA
                                derived from either pooled cytoplasmic polyA RNA from 30
                                cells lines or pooled total RNA from 10 different tissues
                                (from BD Biosciences/Clontech and Washington University).
                                PCR products are directionally cloned into the loxP sites
                                of the pDNR-Dual vector. Library constructed by Dr.
                                Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                                Expression Laboratory, Research Technology Program, SAIC
                                Frederick, NCI-Frederick, Frederick, MD 21702). For
                                information on which gene each clone represents, please
                                visit our anonymous ftp site at
                                ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                                a Note: this is a NIH_MGC Library."

ORIGIN

US-10-787-382-5 (1-134) x CD559535 (1-463)

Alignment Scores:
Pred. No.:
Score: 7.98e-43
Percent Similarity: 417.00   Length: 463
Best Local Similarity: 77.04%   Matches: 87
Query Match: 64.44%   Conservative: 17
                        59.91%   Mismatches: 30
                        6   Indels: 1
                                        Gaps: 0

  1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuLeuLeuValAlaLeuGlyAlaAlaThrTyrValSerAlaPhe 20
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 28 ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTTCTTGGAGCTGCCTACGTGTATGCCATC 87

 21 AlaValGluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuLeuSerThrHis 40

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Db  148  CGAACTCTGCTGATACCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCAC   207
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RESULT 9
CD559690/c

LOCUS   CD559690   467 bp   mRNA   linear   EST 19-NOV-2003
DEFINITION AGENCOURT 14496838 NIH MGC 195 Homo sapiens cDNA clone
            IMAGE:6971768 5', mRNA sequence.
ACCESSION   CD559690
VERSION   CD559690.2 GI:38453490
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 467)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585758.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbb-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone Arrayed by: Agencourt Bioscience Corporation
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBKi row: g column: 07
            High quality sequence stop: 467.
FEATURES   Location/Qualifiers
     source   1..467
                     /organism="Homo sapiens"
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                     /note="Vector: pDNR-Dual, Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.

ORIGIN
            Narayan Bhat, Earl Bere III and Hongling Liao (Gene
            Expression Laboratory, Research Technology Program, SAIC
            Frederick, NCI-Frederick, Frederick, MD 21702). For
            information on which gene each clone represents, please
            visit our anonymous ftp site at
            ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presV.dat
            a Note: this is a NIH_MGC Library."

US-10-787-382-5 (1-134) x CD559690 (1-467)

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Qy    1  MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe   20
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Db   383  CCCAGAGAAATTCCCACAAGTGCGATTGGTGAAAGAGAACCTTGGCCACTGCTTTCTACTCAT  324

Qy   41  ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
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Alignment Scores:
Pred. No.:
Score: 8.07e-43   Length: 467
Score: 417.00   Matches: 87
Percent Similarity: 77.04%   Conservative: 17
Best Local Similarity: 64.44%   Mismatches: 30
Query Match: 59.91%   Indels: 1
DB: 6   Gaps: 0

RESULT 10
CD559689/c

LOCUS   CD559689   473 bp   mRNA   linear   EST 19-NOV-2003
DEFINITION AGENCOURT 14496901 NIH MGC 195 Homo sapiens cDNA clone
            IMAGE:6971769 5', mRNA sequence.
ACCESSION   CD559689
VERSION   CD559689.2 GI:38453487
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 473)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585757.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbb-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone Arrayed by: Agencourt Bioscience Corporation

FEATURES
    source

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
/mol_type="mRNA"
Plate: IRBKl row: g column: 08
High quality sequence start: 16
High quality sequence stop: 473.

Location/Qualifiers
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    /lab_host="DH5A (T1 phage-resistant)"
    /clone_lib="NIH_MGC_195"
    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
    loxP-HindIII; Clones from this library have been
    PCR-amplified using gene-specific primers to contain the
    complete open reading frame (based on known gene sequences
    available from NCBI's RefSeq). Template for PCR is cDNA
    derived from either pooled cytoplasmic polyA RNA from 30
    cells lines or pooled total RNA from 10 different tissues
    (from BD Biosciences/Clontech and Washington University).
    PCR products are directionally cloned into the loxP sites
    of the pDNR-Dual vector. Library constructed by Dr.
    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
    Expression Laboratory, Research Technology Program, SAIC
    Frederick, NCI-Frederick, Frederick, MD 21702). For
    information on which gene each clone represents, please
    visit our anonymous ftp site at
    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSv.dat
    a Note: this is a NIH_MGC Library."

ORIGIN

us-10-787-382-5 (1-134) x CD559689 (1-473)

Alignment Scores:
Pred. No.:
Score: 8.22e-43   Length: 473
Percent Similarity: 417.00   Matches: 87
Best Local Similarity: 77.04%   Conservative: 17
Query Match: 64.44%   Mismatches: 30
                           59.91%   Indels: 1
                           6   Gaps: 0

Qy   1   MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   449   ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC   390

Qy   21   AlaValGluAsnProMetAsnArgLeuValAlaLysGluThrGlnLeuLeuSerThrHis   40
           ||||||||| |||||||| ||||||| |||| |||||||
Db   389   CCCACAGAAATTCCCACAAGTGCATTGGTGTAAAGAAGACACTTGGCACTGCTTCTACTCAT   330

Qy   41   ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis   60
           ||||||| |||||||||||||| |||| |||||| |||
Db   329   CGAACTCGTCGGATAGGCCAATGAGAACCTCGTTCCTGTTACCATAAAATCAC   270

Qy   61   GlnLeuCysIleLysGlyValPheGlnGlyIleAspThrLeuLysAsnGlnThrHrAlaHis   80
           ||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   269   CAACTGTGCACTGAAGAAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA   210

Qy   81   GlyGluAlaValAspLysValPheGlnAsnLeuSerLeuLeuGluHisIleGluArg   100
           |||||||||||||||:|||::|||||||||||||||||||||:::||||:||||
Db   209   GGGGGGTACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGACGGC   150

Qy   101   GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGly1   120
           |||||||||||||||:|||:||||::|||||||||||||:|||||||||||||||||
Db   149   CAAAAAAAAAGTGTGGAAGAAGAAACGGAGAGTAAACCAAATTCCTAGACTACCTGCA   120

Qy   120   nValPheLeuGlyValIleAsnThrGluTrpProGluSer   134
           ||||||||||||::|||||||||||||||||||||||||
Db   89   AGAGTTTCTTGGTGTGTAATGACACCGGAGTGGATAATAGAAAGT   47

RESULT 11

CD559536
LOCUS   CD559536   489 bp   mRNA   linear   EST   26-NOV-2003
DEFINITION   AGENCOURT_14496804_NIH_MGC_195 Homo sapiens cDNA clone
               IMAGE:6971768 5', mRNA sequence.
ACCESSION   CD559536
VERSION   CD559536.2 GI:38558953
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 489)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 10, 2003 this sequence version replaced gi:31585604.
               Contact: Daniela S. Gerhard, Ph.D.
               Office of Cancer Genomics
               National Cancer Institute / NIH
               Bldg. 31 Rm10A07 Bethesda, MD 20892
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Narayan Bhat
               cDNA Library Preparation: Bhat Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov

FEATURES
    source

Plate: IRBKl row: g column: 07
High quality sequence start: 489.
High quality sequence stop: 489.

Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:6971768"
    /tissue_type="mixed"
    /lab_host="DH5A (T1 phage-resistant)"
    /clone_lib="NIH_MGC_195"
    /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
    loxP-HindIII; Clones from this library have been
    PCR-amplified using gene-specific primers to contain the
    complete open reading frame (based on known gene sequences
    available from NCBI's RefSeq). Template for PCR is cDNA
    derived from either pooled cytoplasmic polyA RNA from 30
    cells lines or pooled total RNA from 10 different tissues
    (from BD Biosciences/Clontech and Washington University).
    PCR products are directionally cloned into the loxP sites
    of the pDNR-Dual vector. Library constructed by Dr.
    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
    Expression Laboratory, Research Technology Program, SAIC
    Frederick, NCI-Frederick, Frederick, MD 21702). For
    information on which gene each clone represents, please
    visit our anonymous ftp site at
    ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSv.dat
    a Note: this is a NIH_MGC Library."

ORIGIN

us-10-787-382-5 (1-134) x CD559536 (1-489)

Alignment Scores:
Pred. No.:
Score: 8.61e-43   Length: 489
Percent Similarity: 417.00   Matches: 87
Best Local Similarity: 77.04%   Conservative: 17
Query Match: 64.44%   Mismatches: 30
                           59.91%   Indels: 1
                           6   Gaps: 0

Qy   1   MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaAlaTyrValSerAlaPhe   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   54   ATGAGGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC   113

RESULT 12

BC069137

LOCUS   BC069137   817 bp   mRNA   linear   HTC 26-APR-2004
DEFINITION   Homo sapiens cDNA clone IMAGE:7216996, containing frame-shift
              errors.
ACCESSION   BC069137
VERSION   BC069137.1 GI:46575644
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 817)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
              Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
              Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
              Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
              Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
              Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
              Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
              Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
              Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
              McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
              Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
              Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
              Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
              Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
              Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
              Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
              Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
              Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE   Generation and initial analysis of more than 15,000 full-length
              human and mouse cDNA sequences
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED   12477932
REFERENCE   2 (bases 1 to 817)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2004) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Anup Madan, University of Iowa
              cDNA Library Preparation: Anup Madan, University of Iowa
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Neurogenomics Research Lab,
              200 B EMRB, University of Iowa, Iowa City, IA-52242
              anup-madan@uiowa.edu
              Jessica Fahey, Tim Nelson, Jae Goon Yoon and Anup Madan
              Clone distribution: MGC clone distribution information can be found
              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
              Series: Plate: Row: Column: 0
              This clone has the following problem: frame shifted.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7216996"
                     /tissue_type="Synthetic constructs"
                     /clone_lib="NIH_MGC_243"
                     /lab_host="TOP10"
                     /notes="Vector: pCR Blunt II TOPO"
ORIGIN

US-10-787-382-5 (1-134) × BC069137 (1-817)

Alignment Scores:
Pred. No.:   1.77e-42
Score: 417.00   Length: 817
Percent Similarity: 77.04%   Matches: 87
Best Local Similarity: 64.44%   Conservative: 17
Query Match: 59.91%   Mismatches: 30
DB: 3   Indels: 1
                                      Gaps: 0

Qy   1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaThrTyrValSerAlaPhe 20
          ||| |:: |||||::||||:||:||| :||| :|:|:|:
Db   45 ATGAGGAGGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCCTAGGTGTATGCCATC 104

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 40
          ||| :::
Db 105 CCCACAGAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT 164

Qy   41 ArgThrTrpLeuIleGlyAlaAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
          |||| :::
Db 165 CGAACTCTGCTGATACCCAATGAGACTCTGAGGATTCCGTTCCTGTACATAAAAATCAC 224

Qy   61 GlnLeuCysIleLeuLysGlyValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAlaHis 80
          |||:||| |||:|||||:|:||
Db 225 CAACTGTGCACTGAAGAAATCTTTCAGGGAAATAGGCACACTGGAGTCAAACTGTGCAA 284

Qy   81 GlyGluAlaValAspPheGlnAsnLeuSerLeuLeuLysGluHisIleGluArg 100
          |||:|| :::::
Db 285 GGGGGTACTGTGGAAAGACTATTCAAAAAACTTGTCCTTAATAAAAGAATACAC 344

Qy 101 GlnLeuLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrTyrLeuGl 120
          ||| | |:::| :::||||||
Db 345 CAAAAAGAAAAAGTGTGGAGAAGAGACGGAGAGTAAACCAATTCCTAGACTACCTGCA 404

Qy 120 nValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
          |||||
Db 405 AGAGTTTCTTGGTGTGATTAATGAACACCGAGTGGATAAATAGAAAGT 447

RESULT 13

AY412021

LOCUS   AY412021   405 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION   Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
              genomic survey sequence.
ACCESSION   AY412021
VERSION   AY412021.1 GI:39767986
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 405)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

```
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE   2  (bases 1 to 405)
AUTHORS     Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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     gene            <1..>405
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                     /locus_tag="HCM4418"
ORIGIN
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Alignment Scores:
Pred. No.:                    3.88e-42
Score:                        411.00
Percent Similarity:           75.37%          Matches:         405
Best Local Similarity:        63.43%          Conservative:     85
Query Match:                  59.05%          Mismatches:       16
DB:                           9              Indels:           33
                                              Gaps:              0
                                              Length:          405
```

US-10-787-382-5 (1-134) x AY412021 (1-405)

```
Qy    1 MetArgMetLeuLeuAsnLeuSerLeuLeuAlaLeuGlyAlaAlaThrValSerAlaPhe 20
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Db    1 ATGAGGATGCTTCTCGCAATTCGAGTTTGCTAGCTCTGGAGCTGCCTACGTCATGGCAATC 60

Qy   21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 40
        ||||||:|||||||||||||:::|||||||||||||||||||||||||||||||||||
Db   61 CCCACAGAAATCCCACAAGTGCATGGGTGAAGAGAGACCTTGGCACTGCTTCTCACTCAT 120

Qy   41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
        ||||:||
Db  121 CGAACTCTGCTAATACGCAATCGAGACTCCTGAGGATTCCTGTTCCCTGTACAAAAATCAC 180

Qy   61 GlnLeuCysIleLysGluValPheGlnIleValIleAspPheThrLeuTyrGlnLysGlu 80
        :::||||||||||||:::|||||||||||||:||||||||||||||||::||||||||||
Db  181 CAACNNNNGCACTGAAGAAATCTTTCAGGGAATAAGGCACACTGGACAGAGTCAAACTGCAA 240

Qy   81 GlyGluValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluGluArg 100
        :|||||||||||:::|||||||||:||||
Db  241 GGGGGTACTGTGGAAAAGACTAATCAAAAACTTGTCCTTAATAAAGAAATACATTGAAGGC 300

Qy  101 GlnLysLysArgCysAlaGlyAlaGlyAsnGlyValThrLysSerPheLeuAspTyrLeuGln 120
        |||:|||||||||||||:::||||||||||||||||:::||||:||||||||||
Db  301 CAAAAAAAAAAGTGTGAGGAAGAAGAGGAGAGTAAACCAATTCCTAGACTACCTGCAA 360

Qy  121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
        ||||||||:::|||||||:::|||||||||||||||
Db  361 GAGTTTCTTGGTGTAATACACCGAGTGGATAATAGAAAGT 402
```

US-10-787-382-5 (1-134) x AY412021 (1-405)

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LOCUS       BC066281          456 bp    mRNA     linear    HTC 12-FEB-2004
DEFINITION  Homo sapiens cDNA clone IMAGE:6971770, containing frame-shift
            errors.
ACCESSION   BC066281
VERSION     BC066281.1 GI:42490969
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
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RESULT 14

Second column:

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ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
AUTHORS     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Myers,R.M.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE       Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED      12477932
REFERENCE   2  (bases 1 to 456)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (03-FEB-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: a Column: 17
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 28559032
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971770"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
ORIGIN
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Alignment Scores:
Pred. No.:                    2e-41
Score:                        406.00
Percent Similarity:           76.87%          Matches:         456
Best Local Similarity:        64.93%          Conservative:     87
Query Match:                  58.33%          Mismatches:       16
DB:                           3              Indels:           31
                                              Gaps:              0
                                              Length:          456
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US-10-787-382-5 (1-134) x BC066281 (1-456)

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Qy          1 MetArgMetLeuLeuAsnLeuSerLeuLeuLeuAlaLeuGlyAlaAlaTyrValSerAlaPhe 20
DB         24 ATGAGGATGCTTCTGCATTTGAGTTGCTAGCTGCTCTTGGAGCTGCCTAGCGTGTATGCCATC 83

Qy         21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrThrLeuThrLeuSerThrHis 40
DB         84 CCCACAGAAAATCCCACAAGTGCATTGGTGAAAGAGACCTTGCACTGCTTTCTACTCAT 143

Qy         41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
DB        144 CGAACTCGCTGATTAGCCAATGAGACTTCTGAGGATTCCTGTTCCTGTACATAAAAATCAC 203

Qy         61 GlnLeuCysIleLysGlyGluValPheGlnGlyIleLysAspThrLeuLysAsnGlnThrAlaHis 80
DB        204 CAACTGTGCACTGAAAGAAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 263

Qy         81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuLeuLeuLysGluHisIleGluArg 100
DB        264 GGGGGTACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGA-CGG 322

Qy        101 GlnLysGlyArgCysAlaGlyGlyArgThrArgValThrHisLysPheLeuAspTyrLeuGln 120
DB        323 CCAAAAAAAAGTGTGGAGAAGACGGACGGAGTAAAACCAATTCCTAGACTACCTGCAA 382

Qy        121 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 134
DB        383 GAGTTTCTTGGTGTTAATGAACACCGGAGTGGATAATAGAAAGT 424
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RESULT 15
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LOCUS       CD559688/c
DEFINITION  AGENCOURT 14496964 NIH_MGC_195 Homo sapiens cDNA
            IMAGE:6971770 5', mRNA sequence.
ACCESSION   CD559688
VERSION     CD559688.2  GI:38453486
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585756.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK1 row: 9 column: 09
            High quality sequence start: 11
            High quality sequence stop: 467.
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FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="mixed"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
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ORIGIN
```
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."
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ORIGIN

Alignment Scores:
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Pred. No.:                 2.07e-41
Score:                     406.00      Length:                467
Percent Similarity:        76.87%      Matches:               87
Best Local Similarity:     64.93%      Conservative:          16
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US-10-787-382-5 (1-134) x CD559688 (1-467)

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Qy         21 AlaValGluAsnProMetAsnArgLeuValAlaGluThrThrLeuThrLeuSerThrHis 40
DB        383 CCCACAGAAAATCCCACAAGTGCATTGGTGAAAGAGACCTTGCACTGCTTTCTACTCAT 324

Qy         41 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 60
DB        323 CGAACTCGCTGATTAGCCAATGAGACTTCTGTTCCTGTACATAAAAATCAC 264

Qy         61 GlnLeuCysIleLysGlyGluValPheGlnGlyIleLysAspThrLeuLysAsnGlnThrAlaHis 80
DB        263 CAACTGTGCACTGAAAGAAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 204

Qy         81 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuLeuLeuLysGluHisIleGluArg 100
DB        203 GGGGGTACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGA-CGG 145

Qy        101 GlnLysGlyArgCysAlaGlyGlyArgThrArgValThrHisLysPheLeuAspTyrLeuGln 120
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DB         84 GAGTTTCTTGGTGTTAATGAACACCGGAGTGGATAATAGAAAGT 43
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Search completed: August 7, 2005, 00:10:27
Job time : 2821 secs

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 6, 2005, 19:38:05 ; Search time 2111.1 Seconds
                                              (without alignments)
                                              2639.542 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVAETLTLLST.........PLDYLQVFLGVINTEWTPES 115

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Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416466.

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                10: gb_ro:*
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                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
c 1	610	100.0	345	6	BD211562	Canine an
c 2	610	100.0	345	6	BD211563	Canine an
c 3	610	100.0	345	6	AR241540	Sequence
c 4	610	100.0	345	6	AR241541	Sequence

c	5	610	100.0	345	6	AR254496	Sequence
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c	7	610	100.0	402	6	BD211560	Canine an
c	8	610	100.0	402	6	BD211561	Canine an
c	9	610	100.0	402	6	AR241538	Sequence
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c	13	610	100.0	402	6	AF331919	Canis fam
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	21	601	98.5	405	6	AX083939	Sequence
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	39	357	58.5	864	6	AX766525	Sequence
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ALIGNMENTS

RESULT 1
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LOCUS   BD211562   345 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same.
ACCESSION   BD211562
VERSION   BD211562.1 GI:33021332
KEYWORDS   JP 2002516104-A/68.
SOURCE   Canis familiaris (dog)
  ORGANISM Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same
  JOURNAL   Patent: JP 2002516104-A 68 04-JUN-2002;
            HESKA CORP
COMMENT   OS Canis familiaris (dog)
            PN JP 2002516104-A/68
            PD 04-JUN-2002
            PF 28-MAY-1999 JP JP 2000551002
            PR 29-MAY-1998 US 60/087306
            PI GEKKEB SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
            C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
            PC A61K39/395,
            PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
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FEATURES
source

        Location/Qualifiers
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        /db_xref="taxon:9615"

ORIGIN

US-10-787-382-10 (1-115) x BD211562 (1-345)

Alignment Scores:
Pred. No.:
Score: 8.38e-67   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                        Gaps: 0

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Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
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Qy   41 HisGlnLeuCysIleLysGluValPheGlyGlyIleIleAspThrLeuLysAsnGlnThrAla 60
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Db 121 CACCAACTGTGCATTAAAGAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180

Qy   61 HisGlyGluAlaValAlaAspLysGluLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu 80
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Qy 101 GlnValPheLeuGlyValIleIleAsnThrGluThrTrpThrProGluSer 115
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US-10-787-382-10 (1-115) x BD211563 (1-345)

RESULT 2
LOCUS   BD211563
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same.
ACCESSION   BD211563
VERSION   BD211563.1 GI:33021333
KEYWORDS   JP 200251610-A/69.
SOURCE   Canis familiaris (dog)
  ORGANISM Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory protein, nucleic acid molecules
            and method of using the same
  JOURNAL   Patent: JP 200251610-A 69 04-JUN-2002;
            HESKA CORP
COMMENT   Canis familiaris (dog)
OS   Canis familiaris (dog)
PN   JP 200251610-A/69
PD   04-JUN-2002
PF   28-MAY-1999 US JP 200055100Z
PR   29-MAY-1998 US 60/087306
PI   GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC

LOCUS   BD211563/c
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same.

PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N15/21,C12N5/10, PC
      G01N33/15,
PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
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CC   method of using the same
FH   Key   Location/Qualifiers
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PC   C07K14/54,
PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
      G01N33/15,
PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
      and feline immunoregulatory proteins, nucleic acid CC
      molecules and
CC   method of using the same
FH   Key   Location/Qualifiers
FT   source 1..345
             Location/Qualifiers
             1..345
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FEATURES
source

        Location/Qualifiers
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ORIGIN

US-10-787-382-10 (1-115) x BD211563 (1-345)

Alignment Scores:
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Score: 8.38e-67   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 6   Indels: 0
                                        Gaps: 0

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
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Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
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Db 225 CACCAACTGTGCATTAAAGAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

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Db 165 CACGGGGAGGCTGTGGATAAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysLysArgCysAlaGlyValGlyArgTrpArgValThrLysPheLeuAspTyrLeu 100
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Qy 101 GlnValPheLeuGlyValIleIleAsnThrGluThrTrpThrProGluSer 115
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Db   45 CAAGTATTTCTTGGGTGTAATAAACACCGGAGTGGGACACCGGAAAGT 1

RESULT 3
LOCUS   AR241540
DEFINITION Sequence 85 from patent US 6471957.
ACCESSION   AR241540
VERSION   AR241540.1 GI:27287249
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 85 29-OCT-2002;
FEATURES   Location/Qualifiers
source   1..345
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ORIGIN

Alignment Scores:
Pred. No.:
Score: 8.38e-67   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
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US-10-787-382-10 (1-115) x AR241540 (1-345)

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Db    1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGACACTGCTCTCCACT 60

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAT 120

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
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Qy   81 ArgGlnLysLysSerArgCysAlaGlyGlyAlaGlyValThrLysSerPheLeuAspTyrLeu 100
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Qy  101 GlnValPheLeuGlyValIleIleAsnThrGluTrpThrProGluSer 115
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Db  301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCCGGAAAGT 345
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RESULT 4
LOCUS   AR241541/c
                AR241541   Sequence 87 from patent US 6471957.
DEFINITION   AR241541   345 bp   DNA   linear   PAT 20-DEC-2002
ACCESSION   AR241541
VERSION   AR241541.1   GI:27287250
KEYWORDS
SOURCE   Unknown.
  ORGANISM   Unknown.
               Unclassified.
REFERENCE   1   (bases 1 to 345)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6471957-A 87 29-OCT-2002;
FEATURES   Location/Qualifiers
  source   1. .345
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ORIGIN

Alignment Scores:
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Score: 8.38e-67   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
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US-10-787-382-10 (1-115) x AR241541 (1-345)

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Db    1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGACACTGCTCTCCACT 60

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAT 120

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345 TTTGCTGTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Db  285 CATCGAACTTGGCTGTATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAT 226
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RESULT 5
LOCUS   AR254496/c
                AR254496   Sequence 85 from patent US 6482403.
DEFINITION   AR254496   345 bp   DNA   linear   PAT 20-DEC-2002
ACCESSION   AR254496
VERSION   AR254496.1   GI:27303384
KEYWORDS
SOURCE   Unknown.
  ORGANISM   Unknown.
               Unclassified.
REFERENCE   1   (bases 1 to 345)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 85 19-NOV-2002;
FEATURES   Location/Qualifiers
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ORIGIN

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Qy   61 HisGlyGluValAlaValAspLysAlaGlyGlnLeuAsnLeuSerLeuIleLysGluHisIleGlu 80
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Db  165 CACGGGGAGGCTGTGGATAAAGCTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysLysSerArgCysAlaGlyGlyAlaGlyValThrLysSerPheLeuAspTyrLeu 100
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Db  105 CGCCAAAAAAAAAGGTGTGCAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 46

Qy  101 GlnValPheLeuGlyValIleIleAsnThrGluTrpThrProGluSer 115
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCCGGAAAGT 1
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Alignment Scores:
Pred. No.:
Score: 8.38e-67   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                      Gaps: 0

US-10-787-382-10 (1-115) x AR254496 (1-345)

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Qy    1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
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Db    1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACACTGACACTGCTCTCCACT 60

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAT 120

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CACCAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACACTAGCC 180

Qy   61 HisGlyGluValAlaValAspLysAlaGlyGlnLeuAsnLeuSerLeuIleLysGluHisIleGlu 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CACGGGGAGGCTGTGGATAAAGCTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 240

Qy   81 ArgGlnLysLysSerArgCysAlaGlyGlyAlaGlyValThrLysSerPheLeuAspTyrLeu 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CGCCAAAAAAAAAGGTGTGCAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300

Qy  101 GlnValPheLeuGlyValIleIleAsnThrGluTrpThrProGluSer 115
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCCGGAAAGT 345
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RESULT 6
                AR254497/c
LOCUS   AR254497   345 bp   DNA   linear   PAT 20-DEC-2002

DEFINITION   Sequence 87 from patent US 6482403.
ACCESSION   AR254497
VERSION   AR254497.1 GI:27303385
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 87 19-NOV-2002;
FEATURES   Location/Qualifiers
     source   1..345
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

US-10-787-382-10 (1-115) x AR254497 (1-345)

Alignment Scores:
  Pred. No.:   1.
  Score: 8.38e-67
  Percent Similarity: 610.00
  Best Local Similarity: 100.00%   Length: 345
                            100.00%   Matches: 115
  Query Match: 100.00%   Conservative: 0
  DB: 6   Mismatches: 0
                                           Indels: 0
                                           Gaps: 0

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy   21 HisArgThrThrProLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 285 CATCGAACTACGCCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy   41 HisGlnLeuCysIleLysGluValValPheGlnGlyIleLysAspThrLeuLysAsnGlnThrAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 225 CACCAACTGTGCATTAAAGAAGTTGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy   61 HisGlyGluAlaValAlaSplyLysLeuPheGluAsnLeuSerLeuIleLysGluHisIleGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 165 CACGGGGGAGGCTGTGGATAAACTAATTCCAAAACTGTCTTAATAAAAGAACACAATAGAG 106

Qy   81 ArgGlnLysGlyArgCysAlaGlyValThrArgTrpArgValThrLysPheLeuAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 105 CGCCAAAAAAAAGGTGTGCGAGGGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 46

Qy 101 GlnValPheLeuGlyValIleAsnThrGluThrProThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCGGAAAGT 1

FEATURES   Location/Qualifiers
     source   1..402
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
ORIGIN

US-10-787-382-10 (1-115) x BD211560 (1-402)

Alignment Scores:
  Pred. No.:   1.
  Score: 1.01e-66
  Percent Similarity: 610.00
  Best Local Similarity: 100.00%   Length: 402
                            100.00%   Matches: 115
  Query Match: 100.00%   Conservative: 0
  DB: 6   Mismatches: 0
                                           Indels: 0
                                           Gaps: 0

RESULT 7
BD211560
LOCUS   BD211560   402 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same.
ACCESSION   BD211560
VERSION   BD211560.1 GI:33021330
KEYWORDS   JP 2002516104-A/66.
SOURCE   Canis familiaris (dog)
  ORGANISM   Canis familiaris
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 402)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same
  JOURNAL   Patent: JP 2002516104-A 66 04-JUN-2002;
HESKA CORP
OS   Canis familiaris (dog)
PN   JP 2002516104-A/66
PD   04-JUN-2002
PF   28-MAY-1999 JP 2000551002

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

Qy   21 HisArgThrThrProLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118 CATCGAACTACGCCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 177

Qy   41 HisGlnLeuCysIleLysGluValValPheGlnGlyIleLysAspThrLeuLysAsnGlnThrAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 CACCAACTGTGCATTAAAGAAGTTGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237

Qy   61 HisGlyGluAlaValAlaSplyLysLeuPheGluAsnLeuSerLeuIleLysGluHisIleGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 CACGGGGGAGGCTGTGGATAAACTAATTCCAAAACTGTCTTAATAAAAGAACACAATAGAG 297

Qy   81 ArgGlnLysGlyArgCysAlaGlyValThrArgTrpArgValThrLysPheLeuAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 CGCCAAAAAAAAGGTGTGCGAGGGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 357

Qy 101 GlnValPheLeuGlyValIleAsnThrGluThrProThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||
Db 358 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCGGAAAGT 402

RESULT 8
BD211561/c
LOCUS   BD211561   402 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same.
ACCESSION   BD211561
VERSION   BD211561.1 GI:33021331
KEYWORDS   JP 2002516104-A/67.
SOURCE   Canis familiaris (dog)
  ORGANISM   Canis familiaris
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 402)
  AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules
             and method of using the same
  JOURNAL   Patent: JP 2002516104-A 67 04-JUN-2002;

COMMENT

OS   Canis familiaris (dog)
PN   JP 2002516104-A/67
PD   04-JUN-2002
PF   28-MAY-1999 JP 2000551002
PR   29-MAY-1998 US 60/087306
PI   GEKKEE SIM, SHUMIN YANG, MATHEW J DRBITZ, RAMANI S WONDERLING PC
      C12N15/09,A61K39/395,
PC   A61K39/395,
PC   A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC   C07K14/54,
PC   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
      G01N33/15,
PC   G01N33/50,C12N15/00,A61K37/02,A61K37/04,A61K38/00,A61K39/00,A61K39/395,
PC   G01N33/15,A61K31/7088,A61K38/21,A61K39/00,A61K39/395,
PC   A61K39/395,
PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC   Canine
      and feline immunoregulatory proteins, nucleic acid CC
      molecules and
CC   method of using the same
FH   Key   Location/Qualifiers
FT   source   1..402
FT   /organism="Canis familiaris (dog)".

FEATURES
      source   Location/Qualifiers
                      1..402
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9615"

ORIGIN

Alignment Scores:
Pred. No.:   1.01e-66
Score: 610.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

US-10-787-382-10 (1-115) x BD211561 (1-402)

Qy   1   PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr   20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGACTTCCTACTCCCTGAAAATAAAAAT 226

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy   61 HisGlyGluAlaValAlaAspLysValPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 CACGGGGAGGCTGTGGATAAAGTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysGlySerArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 CGCCAAAAAAAAGGTGTGCGAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG   46

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 9
LOCUS   AR241538
DEFINITION   Sequence 83 from patent US 6471957.
ACCESSION   AR241538
VERSION   AR241538.1 GI:27287247
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 402)
AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL   Patent: US 6471957-A 83 29-OCT-2002;
FEATURES   Location/Qualifiers
  source   1..402
            /organism="unknown"
            /mol_type="unknown"

ORIGIN

Alignment Scores:
Pred. No.:   1.01e-66
Score: 610.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

US-10-787-382-10 (1-115) x AR241538 (1-402)

Qy   1   PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr   20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGACTTCCTACTCCCTGAAAATAAAAAT 177

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237

Qy   61 HisGlyGluAlaValAlaAspLysValPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 CACGGGGAGGCTGTGGATAAAGTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 297

Qy   81 ArgGlnLysGlySerArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 CGCCAAAAAAAAGGTGTGCGAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 357

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||
Db   358 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 10
AR241539/c
LOCUS   AR241539
DEFINITION   Sequence 84 from patent US 6471957.
ACCESSION   AR241539
VERSION   AR241539.1 GI:27287248
KEYWORDS   Unknown.
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 402)
AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE   Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL   Patent: US 6471957-A 84 29-OCT-2002;
FEATURES   Location/Qualifiers
  source   1..402
                /organism="unknown"
                /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.:   1.01e-66
Score: 610.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

US-10-787-382-10 (1-115) x AR241539 (1-402)

Qy   1   PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr   20

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Qy    345 TTTGCTGTAGAAAAATCCCATGAATAGAACTCGGTCGGCGAGAGACCTGACACTGCTCTCCACT 286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 CATCCGAACTTGGCTGATAGGCGATGGGAACCTGATGAATTCCTACTCCCTGAAAATAAAAAT 226

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy     41 HisGlnLeuCysIleLysGluValPheGlnLysAsnLeuSerLeuIleLeuGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACGGGGGAGGCTGTGGATAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 106

Qy     61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 CGCCAAAAAAAAGGTGTGCAGGAGAGATGGGAGAAAGTTCCTAGACTACCTG 46

Qy    101 GlnValPheLeuGluGlyValIleAspAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1
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RESULT 11
LOCUS       AR254494           402 bp    DNA     linear    PAT 20-DEC-2002
DEFINITION  Sequence 83 from patent US 6482403.
ACCESSION   AR254494
VERSION     AR254494.1 GI:27303382
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 83 19-NOV-2002;
FEATURES             Location/Qualifiers
     source          1..402
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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US-10-787-382-10 (1-115) x AR254494 (1-402)

Alignment Scores:
  Pred. No.:
  Score:              1.0e-66
  Percent Similarity: 610.00
  Best Local Similarity: 100.00%         Matches:    115
  Query Match:        100.00%            Conservative: 0
  DB:                 6                  Mismatches: 0
                                         Indels:     0
                                         Gaps:       0
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Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TTTGCTGTAGAAAATCCCATGAATAGAACTCGGTCGGCGAGAGACCTGACACTGCTCTCCACT 286

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 CATCCGAACTTGGCTGATAGGCGATGGGAACCTGATGAATTCCTACTCCCTGAAAATAAAAAT 226

Qy     41 HisGlnLeuCysIleLysGluValPheGlnLysAsnLeuSerLeuIleLeuGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CACGGGGGAGGCTGTGGATAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 297

Qy     61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237

Qy    118 CATCCGAACTTGGCTGATAGGCGATGGGAACCTGATGAATTCCTACTCCCTGAAAATAAAAAT 177

Qy     81 ArgGlnLeuLysGluArgCysAlaGlyGluValArgArgValThrArgLysPheLeuAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 CACGGGGGAGGCTGTGGATAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 297

Qy    101 GlnValPheLeuGluGlyValIleAspAsnThrGluTrpThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 CGCCAAAAAAAAGGTGTGCAGGAGAGATGGGAGAAAGTTCCTAGACTACCTG 357
```

```
Qy    101 GlnValPheLeuGluGlyValIleAspAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 402
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RESULT 12
LOCUS       AR254495/c         402 bp    DNA     linear    PAT 20-DEC-2002
DEFINITION  Sequence 84 from patent US 6482403.
ACCESSION   AR254495
VERSION     AR254495.1 GI:27303383
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  TITLE     Caniney IL-13 immunoregulatory proteins and uses thereof
  JOURNAL   Patent: US 6482403-A 84 19-NOV-2002;
FEATURES             Location/Qualifiers
     source          1..402
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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US-10-787-382-10 (1-115) x AR254495 (1-402)

Alignment Scores:
  Pred. No.:
  Score:              1.0e-66
  Percent Similarity: 610.00
  Best Local Similarity: 100.00%         Matches:    115
  Query Match:        100.00%            Conservative: 0
  DB:                 6                  Mismatches: 0
                                         Indels:     0
                                         Gaps:       0
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```
Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TTTGCTGTAGAAAAATCCCATGAATAGAACTCGGTCGGCGAGAGACCTGACACTGCTCTCCACT 286

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 CATCCGAACTTGGCTGATAGGCGATGGGAACCTGATGAATTCCTACTCCCTGAAAATAAAAAT 226

Qy     41 HisGlnLeuCysIleLysGluValPheGlnLysAsnLeuSerLeuIleLeuGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy     61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACGGGGGAGGCTGTGGATAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 106

Qy     81 ArgGlnLeuLysGluArgCysAlaGlyGluValArgArgValThrArgLysPheLeuAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 CGCCAAAAAAAAGGTGTGCAGGAGAGATGGGAGAAAGTTCCTAGACTACCTG 46

Qy    101 GlnValPheLeuGluGlyValIleAspAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1
```

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RESULT 13
LOCUS       AF331919           610 bp    mRNA    linear    MAM 04-OCT-2001
DEFINITION  Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION   AF331919
VERSION     AF331919.1 GI:15919180
KEYWORDS
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Yang,S., Selins,K.S., Weber,E. and McCall,C.
  TITLE     Canine interleukin-5: molecular characterization of the gene and
            expression of biologically active recombinant protein
```

Left column

JOURNAL   J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
MEDLINE   21334408
PUBMED   11440633
REFERENCE   2 (bases 1 to 610)
AUTHORS   Yang,S.
TITLE   Direct Submission
JOURNAL   Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
   Prospect Parkway, Ft Collins, CO 80525, USA
FEATURES   Location/Qualifiers
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ORIGIN

US-10-787-382-10 (1-115) x AF331919 (1-610)

Alignment Scores:
Pred. No.:
Score: 1.66e-66
Percent Similarity: 610.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

Length: 610
Matches: 115
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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Qy    1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr  20
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Db   86 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla  60
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Db  266 CACGGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 325

Qy   81 ArgGlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPhePheLeuAspTyrLeu 100
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Db  326 CGCCAAAAAAAAAGGTGTGGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 385

Qy  101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||||||
Db  386 CAAGTATTTCTTGGTGTTAATAAACACCGAGTGGACACCGGAAAGT 430
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Right column

AUTHORS   Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE   Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL   Patent: JP 2002516104-A 64 04-JUN-2002;
   HESKA CORP
COMMENT   OS   Canis familiaris (dog)
   PN   JP 200251610A-A/64
   PD   04-JUN-2002
   PF   28-MAY-1999 JP 200551002
   PR   29-MAY-1998 US 60/087306
   PI   GEKKEB SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
   C12N15/09,A61K31/7088,A61K38/00,A61K39/395, PC
   A61K39/395, PC
   A61K45/00,A61K48/00,A61P37/02,A61K38/21,A61K39/00,C07K14/535, PC
   C07K14/54, PC
   C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
   G01N33/15, PC
   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00   Canine
   CC   method of using the same   CC
   FH   Key   Location/Qualifiers
   FT   CDS   Location/Qualifiers
FEATURES   Location/Qualifiers
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ORIGIN

US-10-787-382-10 (1-115) x BD211558 (1-610)

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Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6

Length: 610
Matches: 115
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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Db   86 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
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Db  146 CATCGAACTTGGCTGATAGGCGATGGGAATCTCATGATAATTCCTACTCCTGAAAATAAAAAT 205

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla  60
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Db  206 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265

Qy   61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu  80
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Db  266 CACGGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 325

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Db  326 CGCCAAAAAAAAAGGTGTGGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 385

Qy  101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
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RESULT 15
BD211559/c
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DEFINITION   Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
ACCESSION   BD211559
VERSION   BD211559.1   GI:33021329
KEYWORDS   JP 200251610A-A/65.
SOURCE   Canis familiaris (dog)

Bottom-left column

RESULT 14
BD211558
LOCUS   BD211558   610 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
ACCESSION   BD211558
VERSION   BD211558.1   GI:33021328
KEYWORDS   JP 200251610A-A/64.
SOURCE   Canis familiaris
ORGANISM   Canis familiaris
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 610)

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ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 610)
AUTHORS     Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE       Canine and feline immunoregulatory proteins, nucleic acid molecules
            and method of using the same
JOURNAL     Patent: JP 2002516104-A 65 04-JUN-2002;
            HESKA CORP
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002516104-A/65
            PD   04-JUN-2002
            PF   28-MAY-1999 JP 2000551002
            PR   29-MAY-1998 US           60/087306
            PI   GBKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
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            PC   G01N33/15,
            PC   G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC    Canine
            and feline immunoregulatory proteins, nucleic acid CC
            molecules and
            CC   method of using the same
FEATURES    Key             Location/Qualifiers
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ORIGIN
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US-10-787-382-10 (1-115) x BD211559 (1-610)

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Pred. No. :
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Percent Similarity:         610.00          Matches:          115
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Query Match:                100.00%         Mismatches:       0
DB:                         6               Indels:           0
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Qy    21 HisArgThrTrpIleuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db   465 CATCGAAACTTGGCCTGATAGGCGATGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAAT 406

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Db   285 CGCCAAAAAAAAGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 226

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db   225 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCGGAAAGT 181
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 6, 2005, 19:27:15 ; Search time 314.518 Seconds
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Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVABTLTLLST.............FLDYLQVFLGVINTEWTPES 115

Scoring table: BLOSUM62
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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SUMMARIES

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c 2   610   100.0   345   3   Aaz55551   Canine ma
c 3   610   100.0   402   3   Aaz55548   Canine in
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c 5   610   100.0   610   3   Aaz55546   Canine in

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

[right column]

c 6   610   100.0   610   3   Aaz55547   Canine in
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  34   347   56.9   1533 1   Aan82431   B cell di
  35   347   56.9   1534 2   Aat88013   Murine In
  36   347   56.9   1623 2   Aat14925   T cell re
  37   347   56.9   1623 2   Aav64062   Plasmid p
  38   346   56.7   402   1   Aan81380   A human B
  39   343   56.2   252   4   Aaf74305   Canine in
  40   343   56.2   342   2   Aat14923   T cell re
  41   342   56.1   339   2   Aat14924   T cell re
  42   332.5   54.5   381   2   Aac68867   Modified
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[far right column]

Aaz55547 Canine in
Aaf74300 Canine in
Aaf74306 Canine in
Aaz44265 Porcine I
Aat50756 Ovine IL-
Aat50755 Ovine IL-
Aan91647 Synthetic
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Aaa13338 Human int
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Acf63368 Human int
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Aal61296 hIL5.37 v
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Aav64062 Plasmid p
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ALIGNMENTS

RESULT 1
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ID   AAZ55550 standard; cDNA; 345 BP.
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AC   AAZ55550;
XX
DT   14-MAR-2000 (first entry)
XX
DE   Canine mature interleukin-5 (IL-5) cDNA.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; an.
OS   Canis familiaris.
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999;   99WO-US011942.
XX
PR   29-MAY-1998;   98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58220.

`

.

XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS Claim 1h; Page 226-227; 264pp; English.
XX
CC Sequences AA255546-Z55551 represent cDNA sequences encoding canine
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC nucleotides which encode these immunoregulatory proteins. The proteins,
CC their associated nucleic acids, specific antibodies and inhibitors may be
CC used as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g. antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targetting
XX
SQ Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 5.61e-70   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 3   Indels: 0
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US-10-787-382-10 (1-115) x AA255550 (1-345)

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Db   1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
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Db   121 CACCAACTGTGCATTAAAGAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180

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Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
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US-10-787-382-10 (1-115) x AA255551 (1-345)

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XX
PN WO961618-A2.
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PD 02-DEC-1999.
XX
PF 28-MAY-1999;   99WO-US011942.
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PR 29-MAY-1998;   98US-0087306P.
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PA (HBSK-) HBSKA CORP.
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PI Sim G,   Yang S, Dreitz MJ, Wonderling RS;
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DR WPI; 2000-072623/06.
DR P-PSDB; AAY58220.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS Claim 1h; Page 228; 264pp; English.
XX
CC Sequences AA255546-Z55551 represent cDNA sequences encoding canine
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC nucleotides which encode these immunoregulatory proteins. The proteins,
CC their associated nucleic acids, specific antibodies and inhibitors may be
CC used as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g. antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targetting
XX
SQ Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 5.61e-70   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 3   Indels: 0
                                        Gaps: 0

US-10-787-382-10 (1-115) x AA255551 (1-345)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CACCAACTGTGCATTAAAGAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy   61 HisGlyGluAlaValAlaSpLysLeuPheGlnAsnLeuSerIleLysGluHisIleGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 CACGGGGAGGCTGTGGCATAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysLysArgCysSerLeuGlyLeuArgTrpArgValThrLysAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 CGCCAAAAAAAAAGGTGTGCAGGGAGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 46

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGTGTGATAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 3
AAZ55548
ID   AAZ55548 standard; cDNA; 402 BP.
XX
AC   AAZ55548;
XX
DT   14-MAR-2000 (first entry)
XX
DE   Canine interleukin-5 (IL-5) cDNA coding region.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999; 99WO-US011942.
XX
PR   29-MAY-1998; 98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58219.
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 225; 264pp; English.
XX
CC   Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
CC   interleukin-5 (IL-5). The invention relates to canine IL-5, canine or
CC   feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC   ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   of activity, while the antibodies may be used in detection, and in drug
CC   targeting.
XX
SQ   Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1
Score: 6.94e-70
Pred. No.:
Score: 610.00
Percent Similarity: 100.00%   Length: 402
Best Local Similarity: 100.00%   Matches: 115
Query Match: 3   Conservative: 0
DB: Mismatches: 0
                                   Indels: 0
                                   Gaps: 0

Qy   US-10-787-382-10 (1-115) x AAZ55548 (1-402)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

RESULT 4
AAZ55549/c
ID   AAZ55549 standard; cDNA; 402 BP.
XX
AC   AAZ55549;
XX
DT   14-MAR-2000 (first entry)
XX
DE   Canine interleukin-5 (IL-5) cDNA coding region complement.
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS   Canis familiaris.
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999; 99WO-US011942.
XX
PR   29-MAY-1998; 98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR   WPI; 2000-072623/06.
DR   P-PSDB; AAY58219.
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 226; 264pp; English.
XX
CC   Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
CC   interleukin-5 (IL-5). The invention relates to canine IL-5, canine or
CC   feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC   ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators

Db   58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 CATCGGAACTTGGCTGATAGGCGGGAACCTGATGATTCCTACACCGGAAAATAAAAAT 177

Qy   41 HisGlnLeuCysIleLysGluValPheGlnLysTyrLysAspThrLeuLysAspAsnGlnIleGlu 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACCGCC 237

Qy   61 HisGlyGluAlaValAlaGluThrLeuAlaLeuLeuSerThrLeuLysGluHisIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 CACGGGGAGGCTGTGGCAGAAACTAAAGAGATGGAAGAGTCCTAGAGTTCATACCTG 297

Qy   81 ArgGlyLysLysArgCysSerAlaGlyGluArgTrpTyrValThrProGluLeuAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 CGCCAAAAAAAAGGGTGTGCAGCAGGGGAAAGATGGAGAGTCCTAGAGACTACCTG 357

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   358 CAAGTATTTCTTGGTGTGATAATAAACACCGAGTGGACACCGGAAAGT 402

CC   of activity, while the antibodies may be used in detection, and in drug
CC   targeting
XX
SQ   Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   6.94e-70
Score: 610.00   Length: 402
Percent Similarity: 100.00%   Matches: 115
Percent Identity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 3   Gaps: 0

US-10-787-382-10 (1-115) x AAZ55549 (1-402)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuSerThr 20
Db 225 CACCAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrArgLeuLysAsnGlnThrAla 60
Db 285 CATCGAACCTGGCCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 345 TTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGAACCTTGACACTGCTCTCCACT 286

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuSerThr 20
Db 345 TTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGAACCTTGACACTGCTCTCCACT 286

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrArgLeuLysAsnGlnThrAla 60
Db 285 CATCGAACCTGGCCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy   61 HisGlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 165 CACCGGGGAGGGCTGTGGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysLysArgCysAlaGlyValThrArgPheLeuAspProTyrLeu 100
Db 105 CGCCAAAAAAAAGGTGTGCAGGAGAGAGATGGACAAAAGTTCCTAGACTACCTG 46

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db   45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCCGGAAAGT 1

Db   Canis familiaris.

FT   Key   Location/Qualifiers
FT   CDS   29..433
FT   /tag= a
FT   /product= "Canine IL-5"
XX
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

DE   Canine interleukin-5 (IL-5) cDNA.
XX
DT   14-MAR-2000 (first entry)
XX
AC   AAZ55546;
XX
ID   AAZ55546 standard; cDNA; 610 BP.
AAZ55546

RESULT 5

Db   45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCCGGAAAGT 1

DR   P-PSDB; AAY58219.
DR   WPI; 2000-072623/06;
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
PA   (HESK-) HESKA CORP.
XX
PR   29-MAY-1998; 98US-0087306P.
XX
PP   28-MAY-1999; 99WO-US011942.
XX
PD   02-DEC-1999.
XX
PN   WO9961618-A2.

XX   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 223-224; 264pp; English.

SQ   Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;
XX
CC   targeting
CC   of activity, while the antibodies may be used in detection, and in drug
CC   of inhibitory therapeutics and to screen for modulators
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   also be used for the recombinant production of a protein, while
CC   response from a co-administered antigen. The nucleotide sequences can
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   may be used to treat autoimmune or infectious diseases including
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC   ligand), canine IL-5, feline interferon-alpha (IFN-alpha)
CC   feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC   interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC   Sequences AAZ55546-255551 represent cDNA sequences encoding canine

Alignment Scores:
Pred. No.:   1.24e-69
Score: 610.00   Length: 610
Percent Similarity: 100.00%   Matches: 115
Percent Identity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 3   Gaps: 0

US-10-787-382-10 (1-115) x AAZ55546 (1-610)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuSerThr 20
Db   86 TTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGAACCTTGACACTGCTCTCCACT 145

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db 146 CATCGAACCTGGCCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 205

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrArgLeuLysAsnGlnThrAla 60
Db 206 CACCAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265

Qy   61 HisGlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 266 CACCGGGGAGGGCTGTGGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 325

Qy   81 ArgGlnLysLysArgCysAlaGlyValThrArgPheLeuAspProTyrLeu 100
Db 326 CGCCAAAAAAAAGGTGTGCAGGAGAGAGATGGACAAAAGTTCCTAGACTACCTG 385

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 386 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCCGGAAAGT 430

Db   Canis familiaris.

DE   Canine interleukin-5 (IL-5) cDNA complement.
XX
DT   14-MAR-2000 (first entry)
XX
AC   AAZ55547;
XX
ID   AAZ55547 standard; cDNA; 610 BP.
AAZ55547/c

RESULT 6

KW   immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
KW   Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX
DE   Canine interleukin-5 (IL-5) cDNA complement.

```
XX
OS   Canis familiaris.
XX
FH   Key            Location/Qualifiers
FT
FT   CDS            complement(178..582)
FT                  /*tag= a
FT                  /product= "Canine IL-5"
XX
PN   WO9961618-A2.
XX
PD   02-DEC-1999.
XX
PF   28-MAY-1999; 99WO-US011942.
XX
PR   29-MAY-1998;  98US-0087306P.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR   WPI; 2000-072623/06;
DR   P-PSDB; AAY58219.
XX
PT   Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT   useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS   Claim 1h; Page 224-225; 264pp; English.
XX
CC   Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
CC   interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC   feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC   ligand), canine IL-5, feline interferon-alpha (IFN-alpha), and
CC   and feline granulocyte macrophage colony-stimulating factor (GMCSF), and
CC   nucleotides which encode these immunoregulatory proteins. The proteins,
CC   their associated nucleic acids, specific antibodies and inhibitors may be
CC   used as vaccines for therapeutic or prophylactic regulation of an immune
CC   response in animals (particularly cats, dogs, horses and humans). They
CC   may be used to treat autoimmune or infectious diseases including
CC   allergies, tumours, inflammation and graft rejection, and to increase the
CC   response from a co-administered antigen. The nucleotide sequences can
CC   also be used for the recombinant production of a protein, while
CC   nucleotide fragments are useful as probes, as amplification primers and
CC   as sources of inhibitory therapeutics (e.g. antisense oligonucleotides).
CC   The proteins may be used to raise antibodies and to screen for modulators
CC   of activity, while the antibodies may be used in detection, and in drug
CC   targeting
XX
SQ   Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;


US-10-787-382-10 (1-115) x AAZ55547 (1-610)

Alignment Scores:

Pred. No.:
Score:                 1.24e-69
Score:                 610.00           Length:         610
Percent Similarity:    100.00%          Matches:        115
Best Local Similarity: 100.00%          Conservative:   0
Query Match:           100.00%          Mismatches:     0
DB:                    3                Indels:         0
                                        Gaps:           0

Qy    1   PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 466

Qy   21   HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465  CATCGGAACTTGGCTGATAGGCGGTAAACCTGATGATTCCTACTCCTGAAAATAAAAAT 406

Qy   41   HisGlnLeuCysIleLeuLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405  CACCAACTGTGTCATTAAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 346

Qy   61   HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   345  CACGGGAGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAAGAACATAGAG 286
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   81   ArgGlnLysLysArgCysAlaGlyGluArgValThrArgArgValThrLysPheLeuAspThrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  CGCCAAAAGAAAAAGGTGTGACAGGAGAATGGAGAGAGTGAACAAAGTTCCTAGACTACCTG 226

Qy   101  GlnValPheLeuGlyValIleAspAsnThrGluTrpThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   225  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 181


RESULT 7
AAF74300
ID   AAF74300 standard; DNA; 405 BP.
XX
AC   AAF74300;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Canine interleukin-5 coding sequence #1.
XX
KW   Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW   inflammatory reaction; ds.
XX
OS   Canis sp.
XX
PN   WO20011049-A2.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000; 2000WO-US021651.
XX
PR   10-AUG-1999;  99US-00371615.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Guo H, Lawton R, Mermer B, Aiyappa AP;
XX
DR   WPI; 2001-191542/19;
DR   P-PSDB; AAB72615.
XX
PT   Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT   generating antibodies which are useful in treating allergies in dogs.
XX
PS   Claim 31; Page 46; 48pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC   cancer and inflammatory reactions in dogs. The present sequence is one
CC   version of the IL-5 coding sequence shown in the specification
XX
SQ   Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;


US-10-787-382-10 (1-115) x AAF74300 (1-405)

Alignment Scores:

Pred. No.:
Score:                 1.04e-68
Score:                 601.00           Length:         405
Percent Similarity:    99.13%           Matches:        114
Best Local Similarity: 99.13%           Conservative:   0
Query Match:           98.52%           Mismatches:     1
DB:                    4                Indels:         0
                                        Gaps:           0

Qy    1   PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58   TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 117

Qy   21   HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118  CATCGGAACTTGGCTGATAGGCGGTAAACCTGATGATTCCTACTCCTGAAAATAAAAAT 177

Qy   41   HisGlnLeuCysIleLeuLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   178  CACCAACTGTGTCATTAAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237
```

```
Qy      61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 CACGGGACGAGCCTGTGGATAAACTATTCCAAAACTTGTCTTAATAAAAGAACACATAGAG 297

Qy      81 ArgGlnLysGluLysArgCysAlaGlyValThrLysAspPheLeuAspTyrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 CGCCAAAAAAAAAAGGTGTGCAAGAAGAAGATGGAGGTAGACAAAGTTCCTAGGACTACCTG 357

Qy     101 GlnValPheLeuGlyValIleIleAsnThrGluTrpThrProGluSer 115
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 CAAGTATTTCTTGGTGTTAATAAACACCGAGTGGACAATGGAAAGT 402

RESULT 8
AAF74306
ID   AAF74306 standard; DNA; 393 BP.
XX
AC   AAF74306;
XX
DT   04-MAY-2001 (first entry)
XX
DE   Canine interleukin-5 coding sequence #3.
KW   Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW   inflammatory reaction; d8.
XX
OS   Canis sp.
XX
PN   WO200111049-A2.
XX
PD   15-FEB-2001.
XX
PF   09-AUG-2000; 2000WO-US021651.
XX
PR   10-AUG-1999; 99US-00371615.
XX
SQ   Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;

The present invention provides the protein and coding sequences of the
canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
cancer and inflammatory reactions in dogs. The present sequence is one
version of the IL-5 coding sequence shown in the specification

CC   Claim 1; Page 35; 48pp; English.
XX
PT   Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT   generating antibodies which are useful in treating allergies in dogs.
XX
DR   WPI; 2001-191542/19.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Guo H, Lawton R, Mermer B, Aiyappa AP;
XX

US-10-787-382-10 (1-115) x AAF74306 (1-393)

Query Match:             84.10%
Best Local Similarity:   97.94%
Percent Similarity:     100.00%          Conservative:        2
Score:                  513.00           Matches:            95
Pred. No.:                2.94e-57        Length:            393

Alignment Scores:
                                         Mismatches:          0
                                         Indels:              0
                                         Gaps:                0

Qy      16 ThrLeuLeuSerThrThrHisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThr 35
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ACACTGCTCTCCACTCATCGAACTTGGCTGATAGGGAATGGGAACCTGATGATTCCTACT 60

Qy      36 ProGluAsnLysAsnHisGlnLeuCysIleLysGluValPheGlyGlyIleAspThrLeu 55
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCTGAAAATAAAAATCACCAACTGTGCATTAAAGAAGTTTTTCAGGTATAGACACATTG 120

Qy      56 LysAsnGlnThrArgAlaHisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIle 75
```

```
Db     121 AAAGAACCAAACTGCCACGGGACGAGCCTGTGGATAAACTATTCCAAAACTGTCTTAATA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      76 LysGluHisIleGluArgGlnLysGluLysArgCysAlaGluGlyValThrLysAspThrLys 95
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AAAGAACACATAGAGCGCCAAAAAGAAAAGGTGTGCAAGAAGAAGATGGAGACAAAG 240

Qy      96 PheLeuAspTyrLeuGlnValPheLeuGlyValIleIleAsnThrGluTrpThr 112
           |||||||||||||:::|||||||||||||||||||:::||
Db     241 TTCCTAGACTACCTGCAAGTATTTCTTGGTGTTAATAAACACCGAGTGGACAGT 291

RESULT 9
AAZ44265
ID   AAZ44265 standard; DNA; 838 BP.
XX
AC   AAZ44265;
XX
DT   31-MAR-2000 (first entry)
XX
DE   Porcine IL-5 DNA.
XX
KW   Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;
KW   teniai cysticercus; gamma interferon; IFN-gamma; interleukin 5; 88.
XX
OS   Sus scrofa.
XX
PN   CN1231339-A.
XX
PD   13-OCT-1999.
XX
PF   29-JAN-1999; 99CN-00113447.
XX
PR   29-JAN-1999; 99CN-00113447.
XX
PA   (UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.
XX
PI   Sun S, Dai J;
XX
DR   WPI; 2000-087904/08.
XX
PT   Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
XX
PS   Claim 3; Page 9; 21pp; Chinese.
XX
SQ   Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;

CC   method of the invention
CC   cysticercosis. This sequence represents the pig IL-5 gene used in the
CC   possesses effective immunological protective function for human and pig
CC   vaccine are stable, and the vaccine is easy to store and transport, and
CC   simple and convenient, the physical and chemical properties of the
CC   production and purification process of said nucleic acid vaccine is
CC   interferon (IFN-gamma) and pork interleukin 5 (IL-5)] genes. The
CC   consisting of three protective antigen genes (cC1, cC3 and cC4) of pig
CC   tenial cysticercus and coexpression unit of related cell factor gamma
CC   of a eukaryotic expression plasmid from fusion transcript expression unit
CC   curing human and pork cysticercosis. The invention involves the formation
CC   This invention describes a novel nucleic acid vaccine for preventing and

US-10-787-382-10 (1-115) x AAZ44265 (1-838)

DB:
Query Match:             83.61%
Best Local Similarity:   84.21%
Percent Similarity:      92.98%          Conservative:       10
Score:                  510.00           Matches:            96
Pred. No.:                2.07e-56        Length:            838

Alignment Scores:
                                         Mismatches:          8
                                         Indels:              0
                                         Gaps:                0

Qy       2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis 21
           |||||||:::::|||||||:|||||||||||:|||||||||||||||||||||
Db     105 GCTGTAGCAAAGTCCCATGAATAGGCTGGTTGGCAGAGACCTTGGCACTGCTCTCCACTCAT 164
```

```
Qy    22  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  41
          |||::|
Db   165  CGAACTCTACTAGGCGACGGGGACCTTGATGATGATTCCTACTCCTTGAACCATAACAATCAC  224

Qy    42  GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAlaAsnGlnThrAlaHis  61
          ||||||||:||
Db   225  CAAACTGTGCATTGAAGAAGTCTTTCAGGGTATAGACACATTAAAGAATCGCACTGTGCCG  284

Qy    62  GlyGluValAlaAspLysAlaPheGlnAsnAsnLeuSerIleUlyLysGluHisIleGluGluArg  81
          |||:|||||:|
Db   285  GGGGAAGTCGCTGTGGAAAAAGCTTTTCCGAAACTTGTCTTTAATAAAAGAACACATAGCCGC  344

Qy    82  GlnLysLysAsnProAlaGlyGlyAsnArgTrpAspArgValThrLysPheLeuAspThrTyrLeuGln  101
          ||||||||:||
Db   345  CAAAAAAAAAAGTGTCGGAGGAGAGTAAAAAGTTCCTTAGACTACCTGCAA  404

Qy   102  ValPheLeuGlyValIleAsnThrGluTrpTrpProGluSer  115
          |||||
Db   405  GTGTTTCTTGGTGTGATAAATACACTGAGTGGACAATCGAAAGT  446
```

RESULT 10

```
ID    AAT50756  standard; cDNA; 399 BP.
XX
AC    AAT50756;
XX
DT    17-OCT-2003  (revised)
DT    24-SEP-1997  (first entry)
XX
DE    Ovine IL-5 cDNA.
XX
OS    Ovis aries.
XX
KW    Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW    livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW    immunosuppression; allergy; reproductive system; growth; early maturity;
KW    antibody; diagnosis; immunopotentiator;
KW    early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW    secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; 88.
XX
OS    Ovis aries.
XX
DB    Ovine IL-5 cDNA.
XX
DT    24-SEP-1997  (first entry)
DT    17-OCT-2003  (revised)
XX
AC    AAT50756;
XX
ID    AAT50756  standard; cDNA; 399 BP.
```

US-10-787-382-10 (1-115) x AAT50756 (1-399)

Alignment Scores:

Pred. No.:	2
Score:	7.34e-54
Percent Similarity:	92.11%
Best Local Similarity:	80.70%
Query Match:	2

Length:	399
Matches:	92
Conservative:	13
Mismatches:	9
Indels:	0
Gaps:	0

Sequence 399 BP; 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;

```
SQ
CC    of cytotoxic cells from thymocytes, also it stimulates production and
CC    secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC    induces production of gamma-interferon by, and proliferation of, T and NK
CC    cells and increases the (non-)specific cytolytic lymphocyte response. The
CC    genetic constructs can also be used for in vitro production of IL-5 or -
CC    12. (Updated on 17-OCT-2003 to standardise OS field)
```

RESULT 11

```
ID    AAT50755  standard; DNA; 520 BP.
XX
AC    AAT50755;
XX
DT    17-OCT-2003  (revised)
DT    24-SEP-1997  (first entry)
XX
DE    Ovine IL-5 gene.
XX
OS    Ovis aries.
XX
KW    Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
KW    livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
KW    immunosuppression; allergy; reproductive system; growth; early maturity;
KW    antibody; diagnosis; immunopotentiator;
KW    early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
KW    secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; 88.
XX
OS    Ovis aries.
XX
FH    Key             Location/Qualifiers
FH
FT    CDS             46..444
FT                    /tag= a
FT                    /product= "Ovine_IL-5"
FT    exon            46..183
FT                    /tag= b
FT                    /number= 1
FT    exon            184..216
FT                    /*tag= c
FT                    /number= 2
FT.
```

```
Qy     2  AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHis  21
          |||:||
Db    55  GCTGTAGAAAAGTNACCATGAAATAGACTGGTGGCAGAGAACCTTGACACTGCTCTCCACCGAT  114

Qy    22  ArgThrTrpLeuIleGlyTyrAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis  41
          :::||||
Db   115  CAAACTGCTGATAGGTGAGTGGGAACCTTGATGATGATTCCTACTCCTACTCCTCAGCATACAAATCAC  174

Qy    42  GlnLeuCysIleLysGluValPheGlnGlyIleLeuAspThrLeuLysAlaAsnGlnThrAlaHis  61
          ||||||||:||
Db   175  CAACTATGCATTGAAGAAGTCTTTCAGGGAATAGACACATTGAAGAATCAAACTGCACA  234

Qy    62  GlyGluValAlaAspLysAlaPheGlnAsnAsnLeuSerIleUlyLysGluHisIleGluGluArg  81
          |||:|||||:|
Db   235  GGGGATGCCTGTGAAAAAAATATTCCGAAACTTGTCTTTAATAAAAGAACTACTAGAGACCTC  294

Qy    82  GlnLysLysAsnProAlaGlyGlyAsnArgTrpAspArgValThrLysPheLeuAspThrTyrLeuGln  101
          ||||||||:||
Db   295  CAAAAAAAGGAAGTGTCGGAGGAGAGTAAAAGATTGGGAAACAATTCCTCGACTACCTGCAA  354

Qy   102  ValPheLeuGlyValIleAsnThrGluTrpTrpProGluSer  115
          |||||
Db   355  GTTTTCCTTGGTGTGATAAACACAGAGTGGACGGATGGAAAGC  396
```

```
PF    14-JUN-1996;  96WO-AU000360.
XX
PR    14-JUN-1995;  95AU-00003502.
PR    27-OCT-1995;  95AU-00006244.
XX
PA    (CSIR )  COMMONWEALTH SCI & IND RES ORG.
XX
PI    Seow H,  Wood P;
XX
PN    WO9700321-A1.
XX
PD    03-JAN-1997.
XX
PF    14-JUN-1996;  96WO-AU000360.
XX
DR    WPI; 1997-077528/07.
DR    P-PSDB; AAW08479.
XX
PS    Claim 6; Page 41-42; 78pp; English.
XX
PT    Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT    adjuvants and to treat or prevent microbial infections in livestock.
XX
CC    The sequences given in AAT50755-56 encode ovine interleukin-5 or -12.
CC    Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC    livestock (esp. cows and sheep), particularly where the animals are
CC    stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC    adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC    subunit or synthetic peptide vaccines). They may also be used to treat
CC    cancer, immunosuppression and allergy, to enhance/suppress the
CC    reproductive system and to promote growth or early maturity. Optionally
CC    interleukin can be delivered from constructs or delivery cells and
CC    antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC    infection. The interleukins are immunopotentiators, especially IL-5
CC    promotes growth of early haematopoietic progenitor cells and generation
```

```
FT   exon            217..345
FT                   /*tag= d
FT                   /number= 3
FT   exon            346..480
FT                   /*tag= e
FT                   /number= 4
XX
PN   WO9700321-A1.
XX
PD   03-JAN-1997.
XX
PF   14-JUN-1996;   96WO-AU000360.
XX
PR   14-JUN-1995;   95AU-00003502.
PR   27-OCT-1995;   95AU-00006244.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Seow H, Wood P;
XX
DR   WPI; 1997-077528/07.
DR   P-PSDB; AAW08479.
XX
PT   Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
PT   adjuvants and to treat or prevent microbial infections in livestock.
XX
PS   Claim 6; Page 39-40; 78pp; English.
XX
CC   The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
CC   Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC   livestock (esp. cows and sheep), particularly where the animals are
CC   stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC   adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC   subunit or synthetic peptide vaccines). They may also be used to treat
CC   cancer, immunosuppression and allergy, to enhance/suppress the
CC   reproductive system and to promote growth or early maturity. Optionally
CC   interleukin can be delivered from constructs or delivery cells and
CC   antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC   infection. The interleukins are immunopotentiators, especially IL-5
CC   promotes growth of early haematopoietic progenitor cells and generation
CC   of cytotoxic cells from thymocytes, also it stimulates production and
CC   secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC   induces production of gamma-interferon by, and proliferation of, T and NK
CC   cells and increases the (non-)specific cytolytic lymphocyte response. The
CC   genetic constructs can also be used for in vitro production of IL-5 or -
CC   12. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;

US-10-787-382-10 (1-115) x AAT50755 (1-520)

Alignment Scores:
Pred. No.:
Score:                  1.06e-53
                        487.00       Length:           520
Percent Similarity:     92.11%       Matches:          92
Percent Similarity:     80.70%       Conservative:     13
Best Local Similarity:  79.84%       Mismatches:       9
Query Match:            2            Indels:           0
DB:                                  Gaps:             0

Qy    2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 21
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 21

Qy  100 GCTGTAGAAAGTACCATGAATAGAGACTTGGTGGCCAGAGACCTTGACACTGCTCCACGCAT 159
        |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GCTGTAGAAAGTACCATGAATAGAGACTTGGTGGCCAGAGACCTTGACACTGCTCCACGCAT 159

Qy   22 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 41
        ::|||   |||||||||::||||||||||||||||||||||||||||||||  |||||||
Db   62 ArgThrTrpLeuIleGlyAsnLeuSerLeuLeuLysGluHisIleGluArg 81

Qy  160 CAAACTCTGCTGATAGGTGATGGGAACTTGATGATTCCTACTCCTTCAGCATACAAATCAC 219
        |||||||||||||   |||::|||||||||||||||||||||||||||||||||||||||
Db   42 GlnLeuCysIleLysGluGlyValPheGlyIleGlyTyrIleAspAspThrHisAlaHis 61

Qy  220 CAAACTATGCCATTGAAGAAGTCTTTCAGGGAATAGACACATTGAAGAATCAAAACTGCACAA 279
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 GlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 81
```

```
Db  280 GGGGATGCTGCTGTGAAAAAAAAAAAATTCCGAAACTTGTCTTTAATAAAAGAATACATAGACCTC 339
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   82 GlnLysLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGln 101
        |||||||:::::||||||
Db  340 CAAAAAAGGAAGTGTGGAGGAGAAGAGAAGAGATGGAAACAATTCCTCGACTACCTGCAA 399

Qy  102 ValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
        ||||||||||||||||||||||||||||||
Db  400 GTTTTCCTTGGTGTGATAAACACAGAGTGGACGATGGAAAGC 441

RESULT 12
AAN91647
ID   AAN91647 standard; DNA; 370 BP.
XX
AC   AAN91647;
XX
PN   GB2217328-A.
XX
DT   25-MAR-2003   (revised)
DT   21-MAR-1990   (first entry)
XX
DT   25-OCT-1989.
XX
PF   12-APR-1988;   88GB-00008524.
XX
PR   12-APR-1988;   88GB-00008524.
XX
PA   (BRBI-) BRITISH BIO-TECHN L.
XX
PI   Edwards RM;
XX
DR   WPI; 1989-311767/43.
DR   P-PSDB; AAP93152.
XX
PT   Synthetic gene encoding human interleukin-5 - has restriction sites at
PT   frequent intervals to facilitate manipulation.
XX
PS   Claim 1; Fig 3a; 21pp; English.
XX
CC   Has sites for HindIII, BspMI, NcoI, SpeI, BspMII, ApaLI, XmnI, XhoI ClaI,
CC   BalI, PstI, DraIII, BamHI and EcoRI. IL5 acts as a B cell growth and
CC   differentiation factor. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 370 BP; 126 A; 73 C; 82 G; 89 T; 0 U; 0 Other;

Key        Location/Qualifiers
CDS        14..352
           /*tag= a

US-10-787-382-10 (1-115) x AAN91647 (1-370)

Alignment Scores:
Pred. No.:
Score:                  1.74e-37
                        361.00       Length:           370
Percent Similarity:     77.19%       Matches:          71
Percent Similarity:     62.28%       Conservative:     17
Best Local Similarity:  59.18%       Mismatches:       26
Query Match:            1            Indels:           0
DB:                                  Gaps:             0

Qy    2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 21
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db    2 AlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHis 21

Qy   11 GCCATGGAAATTCCCACTACAGTCCATTCGGTGAAAGAGACCTTGGCACTGCTTTCTACTCAT 70
        ||||||:||||||||:|||||||||||||||||||||||||||||||||||||
Db    1 ...

Qy   22 ArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHis 41
        |||   ||||||::|||
Db   41 ...

Qy   71 CGAACTTGCTGATAGGCCAATGAGACTCCTCGGATTCCTCGTTCCTGTTACAATAAAAATCAC 130
        |||||   :::   |||
Db   71 ...
```

```
Qy   42  GlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHis 61
         |||:||||||||:|||:||||||||||||||||||||||||||:::||||||:||||
Db   131 CAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGAGAGTCAAACTGTGCAA 190

Qy   62  GlyGluAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArg 81
         ||||||||||||||||||||||||||||||||||||||:::||||||||:|::
Db   191 GGGGGTACGTGGGAAAGACTATTCAAAAACTTGTCCTTAATAAAAGAAAATACATTGAT 250

Qy   82  GlnLysLysArgCysGlnAlaGlyLeuArgTrpArgValThrLysSerPheLeuAspTyrLeuGln 101
         ||||||||||||||||||||||||||||||||||||||
Db   251 CAAAAAAAGTGTGGAGAAGAAAGACGGAGAGTAAACCAATTCCTAGACTACCTGCAG 310

Qy   102 ValPheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
         ||||||||||||||||||||||||||||||||||||||
Db   311 GAGTTTCTTGGTGTGATAATAGAACACCCAGTGGATAATAGAAAGT 352
```

RESULT 13

```
ID   AAL61295 standard; DNA; 864 BP.
XX
AC   AAL61295;
XX
DT   22-SEP-2003  (first entry)
XX
DE   hIL5.36 variant DNA.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
KW   Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW   tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
KW   IL5; epitope; human; tetanus toxoid; chimeric; variant; gene; ds.
XX
FH   Key            Location/Qualifiers
FH
FT   CDS            1..864
FT                  /tag= a
FT                  /product= "hIL5.36 variant protein"
FT   sig_peptide    1..57
FT                  /tag= b
FT                  /note= "Human IL5 leader peptide"
FT   mat_peptide    58..861
FT                  /tag= c
FT                  /product= "Mature hIL5.36 variant protein"
FT   misc_feature   70..132
FT                  /tag= d
FT                  /note= "Tetanus toxoid P30 epitope"
FT   misc_feature   817..861
FT                  /tag= e
FT                  /note= "Tetanus toxoid P2 epitope"
XX
CC   The invention relates to immunogenic analogues of multimeric proteins
CC   such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC   factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC   analogues. The immunogenic analogue is useful for preparing a composition
CC   for treating inflammatory diseases, e.g., arthritis. It is also used in
CC   gene therapy. The present sequence is a variant DNA encoding a fusion
CC   construct which comprises 2 human interleukin 5 (IL5) monomers joined by
CC   diglycine linker and including terminally positioned tetanus toxoid
CC   epitopes P30 and P2. This sequence is used to illustrate the method of
CC   the invention
XX
SQ   Sequence 864 BP; 278 A; 184 C; 201 G; 201 T; 0 U; 0 Other;
```

Example 3; Page 114-115; 196pp; English.

US-10-787-382-10 (1-115) x AAL61295 (1-864)

```
Alignment Scores:
 Pred. No.:                1.88e-36
 Score:                      357.00     Length:          864
 Percent Similarity:         76.99%     Matches:          70
 Best Local Similarity:      61.95%     Conservative:     17
 Query Match:                58.52%     Mismatches:       26
 DB:                              9     Indels:            0
                                        Gaps:              0
```

```
Qy   3   ValGluAsnProMetAsnArgLeuValAlaAlaGluThrLeuThrLeuLeuSerThrHisArg 22
         ||| :: |||    || :::
Db   127 CTGGAGATTCCCACACATGCATTGGTGAAAGAGACCTTGGACACTGCTTTCTACTCATCGA 186

Qy   23  ThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGln 42
         |||||| ||| :::||| :::||||AsnLysAsnHisGln
Db   187 ACTCTCCTGATAGGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCACCAA 246

Qy   43  LeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGly 62
         ||||||||||||||||||||||||||||||||||||
Db   247 CTGTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGAGAGTCAAACTGTGCAAGGG 306

Qy   63  GluAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGln 82
         |||||||||||||||||||||||||||||||:::|||||||:::|||
Db   307 GGTACGTGGGAAAGACTATTCAAAAACTTGTCCTTAATAAAAGAAAATACATTGACGGCCA 366

Qy   83  LysLysArgCysGlnAlaGlyLeuArgTrpArgValThrLysSerPheLeuAspTyrLeuGlnVal 102
         |||||||||||||||||:::||||||||||||||
Db   367 AAAAAAGTGTGGAGAAGAAAGACGGAGAGTAAACCAATTCCTAGACTACCTGCAGAG 426

Qy   103 PheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
         ||||||||||:::||||||||||
Db   427 TTTCTTGGTGTGATAATAGAACACCCAGTGGATAATAGAAAGT 465
```

RESULT 14

```
ID   AAA34857 standard; DNA; 816 BP.
XX
AC   AAA34857;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2546.
XX
OS   Homo sapiens.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
PN   WO2000009525-A2.
```

.

```
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999, 99WO-US017712.
XX
PR   03-AUG-1998; 98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT
PS   Disclosure; Page 716; 1343pp; English.
XX
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

US-10-787-382-10 (1-115) x AAA34857 (1-816)

Alignment Scores:
Pred. No.:
Score:                  2.34e-36
                        356.00              Length:        816
Percent Similarity:     76.79%              Matches:       70
Best Local Similarity:  62.50%              Conservative:  16
Query Match:            58.36%              Mismatches:    26
                                            Indels:        0
                                            Gaps:          0

Qy     4  GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArgThr   23
          ||| ::: ||||||||| |||||||||||||||
Db   111  GAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCATCGAACT  170

Qy    24  TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu   43
          |||||| ::: ||||||||||
Db   171  CTGCTGATTAGCCAATGAGACTTCTGAGGATTCCTGTTCCTGTACTATAAAAATCACCAACTG  230

Qy    44  CysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrArgAlaHisGlyGlu   63
          ||||| ::: ||||||||||| ::: |||||
Db   231  TGCACTGAAGCAGAAATCTTTCAGGGAATAGGACACTCGGAAGAGTCAAAACTGTGCAAGGGGGT  290

Qy    64  AlaValAspValPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys   83
          ||| :::||||| ||||||||| ::: |||||
Db   291  ACTGTGGAAAGACTATTCAAAAAAACTTGTCCTTAATAAAGAAATACATTGACGGCCAAAA  350
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```
Qy    84  LysArgCysAlaGlyGlyAlaArgTrpArgValThrArgLysPheLeuAspTyrLeuGlnValPhe  103
          ||| :::||||||||||||||| :::||||||||
Db   351  AAAAAGTGTGCAGGAGGAAGCAGGGAGAGTAAACCAAATTCCTAGACTACCTGCAAGAGTTT  410

Qy   104  LeuGlyValIleAsnThrGluThrTrpProGluSer  115
          ||| :::||||||||||||||
Db   411  CTTGGTGTAATGAACACCGAGTGGATTAATAGAAAGT  446

RESULT 15
AAA13338
ID   AAA13338 standard; cDNA, 816 BP.
XX
AC   AAA13338;
XX
DT   25-JUL-2000  (first entry)
XX
OS   Homo sapiens.
XX
PN   US6048726-A.
XX
PD   11-APR-2000.
XX
PF   15-MAY-1998;   98US-00079839.
XX
PR   15-MAY-1998;   98US-0079839.
XX
PA   (WELT/) WELTMAN J K.
PA   (KARI/) KARIM A S.
XX
PI   Weltman JK, Karim AS;
XX
DR   WPI; 2000-302784/26.
XX
PT
DE   Human Interleukin-5 (IL-5) nucleotide sequence.
XX
KW   Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;
KW   antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;
KW   allergic conjunctivitis; inhibitor; 88.
XX
PS   Disclosure; Col 3-4; 11pp; English.
XX
CC   This sequence represents the human interleukin-5 (IL-5) encoding
CC   nucleotide sequence. Interleukin-5 is involved in eosinophilic
CC   inflammation and inflammatory disorders. The present invention relates to
CC   an IL-5 antisense oligonucleotide (see AAA13337) which inhibits the
CC   expression of IL-5. The antisense oligonucleotide has at least one non-
CC   natural internucleoside linkage. The oligonucleotide is able to inhibit
CC   IL-5 secretion in a dose dependent manner, and is useful for inhibiting
CC   IL-5 expression and therefore treating inflammatory diseases, asthma,
CC   allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases
CC   such as eczema
XX
SQ   Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                  2.34e-36
                        356.00              Length:        816
Percent Similarity:     76.79%              Matches:       70
Best Local Similarity:  62.50%              Conservative:  16
Query Match:            58.36%              Mismatches:    26
                                            Indels:        0
                                            Gaps:          0

US-10-787-382-10 (1-115) x AAA13338 (1-816)

Qy     4  GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArgThr   23
          ||| :::||||||||||||||||||||||||||
Db   111  GAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCATCGAACT  170
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Qy     24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu  43
          ||||||||                    :::
Db    171 CTGCTCGATAGCCAATGAGACTCTGACGGATTCCCTGTTCCTGTACATAAAAATCACCAACTG 230

Qy     44 CysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu  63
          |||           :::||||||||||||||||||||||        :::::::||||||||
Db    231 TGCACTGAAGAAATCTTTCAGGGAATTAGGCACACTGGAGAGTCAAACTGTGCAAGGGGGGT 290

Qy     64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGluArgGlnLys  83
          |||||::::|||||||||||||||||||||||||||||||||::::||||        |||||||
Db    291 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAAATACATTGACGGGCCAAAAA 350

Qy     84 LysArgCysAlaGlyGluArgTrpArgValThrLysCysPheLeuAspTyrLeuGlnValPhe 103
          ||||::::|||||||||||||            |||||::::||||||||||||||||||||||
Db    351 AAAAAGTGTGGAGAAGGACGGGAGAGTAAACCAATTCCTAGACTACCTCGCAAGAGTTT 410

Qy    104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
          ||||::::||||||||||||||||||
Db    411 CTTGGTGTAATGAACACCGAGTGGGATAAATAGAAAGT 446
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: August 6, 2005, 20:22:55 ; Search time 102.068 Seconds
                                                   (without alignments)
                                                   1843.588 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVAETLTLLST..........FLDYLQVFLGVINTEWTPES 115

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                        Ygapop 10.0 , Ygapext 0.5
                        Fgapop   6.0 , Fgapext 7.0
                        Delop   6.0 , Delext   7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                        Maximum Match 100%
                        Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.		Score	Query Match %	Match Length	DB	ID	Description
1	c	610	100.0	345	4	US-09-322-409-85	Sequence 85, Appl
2	c	610	100.0	345	4	US-09-322-409-87	Sequence 87, Appl
3	c	610	100.0	345	4	US-09-451-527-85	Sequence 85, Appl
4	c	610	100.0	345	4	US-09-451-527-87	Sequence 87, Appl
5	c	610	100.0	402	4	US-09-322-409-83	Sequence 83, Appl
6	c	610	100.0	402	4	US-09-322-409-84	Sequence 84, Appl
7	c	610	100.0	402	4	US-09-451-527-83	Sequence 83, Appl
8	c	610	100.0	402	4	US-09-451-527-84	Sequence 84, Appl
9	c	610	100.0	402	4	US-09-322-409-80	Sequence 80, Appl
10	c	610	100.0	610	4	US-09-451-527-80	Sequence 80, Appl
11	c	610	100.0	610	4	US-09-322-409-82	Sequence 82, Appl
12	c	610	100.0	610	4	US-09-451-527-82	Sequence 82, Appl

13		601	98.5	405	4	US-09-371-615A-1	Sequence 1, Appli
14		356	58.4	816	3	US-09-079-839-2	Sequence 2, Appli
15		351	57.5	377	3	US-09-180-864-1	Sequence 1, Appll
16		350	57.4	816	3	US-09-023-655-1236	Sequence 1236, Ap
17		347	56.9	1534	3	US-08-629-643A-4	Sequence 4, Appli
18		347	56.9	1534	3	US-09-155-884-4	Sequence 4, Appli
19		332.5	54.5	351	4	US-09-556-818-27	Sequence 27, Appl
20		331.5	54.3	399	4	US-09-556-818-39	Sequence 39, Appl
21		330.5	54.2	375	4	US-09-556-818-33	Sequence 33, Appl
22		328.5	53.9	393	4	US-09-556-818-31	Sequence 31, Appl
23		324	53.1	444	4	US-09-556-818-43	Sequence 43, Appl
24		322.5	52.9	393	4	US-09-556-818-41	Sequence 41, Appl
25		321.5	52.7	375	4	US-09-556-818-37	Sequence 37, Appl
26		319.5	52.4	375	4	US-09-556-818-45	Sequence 45, Appl
27		318.5	52.2	393	4	US-09-556-818-55	Sequence 55, Appl
28		315.5	51.7	387	4	US-09-556-818-49	Sequence 49, Appl
29		311	51.0	438	4	US-09-556-818-59	Sequence 59, Appl
30		309.5	50.7	387	4	US-09-556-818-57	Sequence 57, Appl
31		308.5	50.6	369	4	US-09-556-818-53	Sequence 53, Appl
32		301.5	49.4	357	4	US-09-556-818-35	Sequence 35, Appl
33		299.5	49.1	375	4	US-09-556-818-29	Sequence 29, Appl
34		289.5	47.5	351	4	US-09-556-818-51	Sequence 51, Appl
35		287.5	47.1	369	4	US-09-556-818-47	Sequence 47, Appl
36		222	36.4	6727	3	US-08-629-643A-5	Sequence 5, Appli
37		222	36.4	6727	3	US-09-280-799-1	Sequence 5, Appli
38		222	36.4	6727	3	US-09-155-884-5	Sequence 5, Appll
39		215.5	35.3	3230	3	US-09-280-799-78	Sequence 78, Appl
40		215.5	35.3	3230	6	US-5324640-1	Patent No. 5324640
41		215.5	35.3	3230	6	US-5324640-1	Patent No. 5324640
42		215.5	35.3	33140	4	US-09-596-002-23	Sequence 23, Appl
43		75	12.3	75595	4	US-09-949-016-15318	Sequence 15318, A
44		75	12.3	148794	4	US-09-949-016-12751	Sequence 12751, A
45		73	12.0	74353	4	US-09-949-016-15336	Sequence 15336, A

RESULT 1
US-09-322-409-85

; Sequence 85, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-322-409-85

Alignment Scores:
Pred. No.:   1.13e-81
Score: 610.00   Length: 345
Percent Similarity: 100.00%   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: Indels: 0
                                            Gaps: 0

US-10-787-382-10 (1-115) x US-09-322-409-85 (1-345)

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Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db   61 CATCGAACTTGGCTGATAGGCGAACCTGATGAGAATTCCTACTCCTGAAAATAAAAAT 120

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyTyrIleAspThrLeuLysAsnGlnThrAla 60
Db 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180

Qy   61 HisGlyGluAlaValAspProLysPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 181 CACGGGGAGGCTGTGGATCCAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 240

Qy   81 ArgGlnLysGlyArgGlyAlaGlyArgTrpArgValThrLysValThrLysValPheLeuAspTyrLeu 100
Db 241 CGCCAAAAAAAGGGTGTGCAGGAGAGAGATGGACAAAAGTTCCTAGACTACCTG 300

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 345

RESULT 2
US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87

Alignment Scores:
Pred. No.:
Score: 1.13e-81
Percent Similarity: 610.00   Length: 345
Best Local Similarity: 100.00%   Matches: 115
Query Match: 100.00%   Conservative: 0
                        4   Mismatches: 0
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US-10-787-382-10 (1-115) x US-09-322-409-87 (1-345)

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Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysBAsn 40
Db   61 CATCGAACTTGGCTGATAGGCGAACCTGATGAGAATTCCTACTCCTGAAAATAAAAAT 120

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyTyrIleAspThrLeuLysAsnGlnThrAla 60
Db 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 180

Qy   61 HisGlyGluAlaValAspProLysPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 181 CACGGGGAGGCTGTGGATCCGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 240

Qy   81 ArgGlnLysGlyArgGlyAlaGlyArgTrpArgValThrLysValThrLysValPheLeuAspTyrLeu 100
Db 241 CGCCAAAAAAAGGGTGTGCAGGAGAGAGATGGGACAAAAGTTCCTTAGACTACCTG 300

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 345

Db 165 CACGGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysGlyArgGlyAlaGlyArgTrpArgValThrLysValThrLysValPheLeuAspTyrLeu 100
Db 105 CGCCAAAAAAAGGGTGTGCAGGAGAGAGATGGACAAAAGTTCCTAGACTACCTG 46

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
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RESULT 3
US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

Alignment Scores:
Pred. No.:
Score: 1.13e-81
Percent Similarity: 610.00   Length: 345
Best Local Similarity: 100.00%   Matches: 115
Query Match: 100.00%   Conservative: 0
                        4   Mismatches: 0
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US-10-787-382-10 (1-115) x US-09-451-527-85 (1-345)

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Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db   61 CATCGAACTTGGCTGATAGGCGAACCTGATGAGAATTCCTACTCCTGAAAATAAAAAT 120

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyTyrIleAspThrLeuLysAsnGlnThrAla 60
Db 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 180

Qy   61 HisGlyGluAlaValAspProLysPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db 181 CACGGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 240

Qy   81 ArgGlnLysGlyArgGlyAlaGlyArgTrpArgValThrLysValThrLysValPheLeuAspTyrLeu 100
Db 241 CGCCAAAAAAAGGGTGTGCAGGAGAGAGATGGACAAAAGTTCCTAGACTACCTG 300

Qy 101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db 301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 345

RESULT 4
US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THERBOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

Alignment Scores:
Pred. No.:
Score: 1.13e-81   Length: 345
                          610.00   Matches: 115
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 4   Gaps: 0

US-10-787-382-10 (1-115) x US-09-451-527-87 (1-345)

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Db  345  TTTGCTGTAGAAAATCCCATGAATAGACTGGTCGCAGAGAACCTTGACACTCGTCTCCACT  286

Qy  21   HisArgThrTrpLeuIleGlyAsnGlyAsnLeuMetIleProThrProGluAsnLysAsn   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  285  CATCGAACTTGGCTGATAGGCGGTAGGCAACCTGATGATTCCTACTCCTGAAAATAAAAAT  226

Qy  41   HisGlnLeuCysIleLysGluValPheGlnIleGlyIleAspThrLeuLysAsnGlnThrAla   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  225  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC  166

Qy  61   HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleLeuGlu   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  165  CACGGGGAGGCTGTCGATAAACTATTCCAAAACTTGTCTTAATAAAAGAACACATAGAG  106

Qy  81   ArgGlnLysSerArgCysAlaGlyLysGluArgTrpArgValThrLysPheLeuAspTyrLeu  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  105  CGCCAAAAAAAAGGCTGTGCAGGAGAAGATGGGAGGTGACAAAGTTCCTAGACTACCTG   46

Qy  101  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  115
         |||||||||||||||||||||||||||||||||||||||||||||
Db   45  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT    1
```

RESULT 5
US-09-322-409-83
; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

Alignment Scores:
Pred. No.:
Score: 1.43e-81   Length: 402
                          610.00   Matches: 115
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 4   Gaps: 0

US-10-787-382-10 (1-115) x US-09-322-409-83 (1-402)

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Qy   1   PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr   20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58  TTTGCTGTAGAAAATCCCATGAATAGACTGGTCGCAGAGAACCTTGACACTCGTCTCCACT  117

Qy  21   HisArgThrTrpLeuIleGlyAsnGlyAsnLeuMetIleProThrProGluAsnLysAsn   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  118  CATCGAACTTGGCTGATAGGCGGTAGGCAACCTGATGATTCCTACTCCTGAAAATAAAAAT  177

Qy  41   HisGlnLeuCysIleLysGluValPheGlnIleGlyIleAspThrLeuLysAsnGlnThrAla   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC  237

Qy  61   HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleLeuGlu   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238  CACGGGGAGGCTGTCGATAAACTATTCCAAAACTTGTCTTAATAAAAGAACACATAGAG  297

Qy  81   ArgGlnLysSerArgCysAlaGlyLysGluArgTrpArgValThrLysPheLeuAspTyrLeu  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298  CGCCAAAAAAAAGGCTGTGCAGGAGAAGATGGGAGGTGACAAAGTTCCTAGACTACCTG  357

Qy  101  GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer  115
         |||||||||||||||||||||||||||||||||||||||||||||
Db  358  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT  402
```

RESULT 6
US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84

Alignment Scores:
Pred. No.:
Score: 1.43e-81   Length: 402
                          610.00   Matches: 115
Percent Similarity: 100.00%   Conservative: 0

```
Best Local Similarity:      100.00%        Mismatches:     0
Query Match:                100.00%        Indels:         0
DB:                              4         Gaps:           0

US-10-787-382-10 (1-115) x US-09-322-409-84 (1-402)

Qy     1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr       20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  286

Qy    21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CATCGAACTTGGCTGATAGGGGGATGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAT 226

Qy    41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CACCAACTGTGCATTAAAGGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 166

Qy    61 HisGlyGluValAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 CACGGGGAGGCTGTGGATAAAACTATTCCAAAACTTGCTTTAATAAAAGAACACATAGAG 106

Qy    81 ArgGlnLysLysSerArgCysAlaGlyLysGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 CGCCAAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAAGTTCCTAGACTACCTG  46

Qy   101 GlnValPheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
           |||||||||||||||||||||||
Db    45 CAAGTATTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 7
US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
;    APPLICANT: Sim, Gek-Kee
;    APPLICANT: Yang, Shumin
;    APPLICANT: Dreitz, Matthew J.
;    APPLICANT: Wonderling, Ramani S.
;    TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;    TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;    FILE REFERENCE: IM-2-C2
;    CURRENT APPLICATION NUMBER: US/09/451,527
;    CURRENT FILING DATE: 1999-12-01
;    EARLIER APPLICATION NUMBER: 09/322,409
;    EARLIER FILING DATE: 1999-05-28
;    EARLIER APPLICATION NUMBER: 60/087,306
;    EARLIER FILING DATE: 1998-05-29
;    NUMBER OF SEQ ID NOS: 174
;    SOFTWARE: Patentin Ver. 2.0
;    SEQ ID NO 83
;    LENGTH: 402
;    TYPE: DNA
;    ORGANISM: Canis familiaris
US-09-451-527-83

Alignment Scores:
Pred. No.:                 1.43e-81       Length:          402
Score:                      610.00        Matches:         115
Percent Similarity:        100.00%        Conservative:      0
Best Local Similarity:     100.00%        Mismatches:        0
Query Match:               100.00%        Indels:            0
DB:                             4         Gaps:              0

US-10-787-382-10 (1-115) x US-09-451-527-83 (1-402)

Qy     1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr       20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  286

Qy    21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CATCGAACTTGGCTGATAGGGGGATGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAT 226

Qy    41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CACCAACTGTGCATTAAAGGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 166

Qy    61 HisGlyGluValAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 CACGGGGAGGCTGTGGATAAAACTATTCCAAAACTTGCTTTAATAAAAGAACACATAGAG 106

Qy    81 ArgGlnLysLysSerArgCysAlaGlyLysGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 CGCCAAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAAGTTCCTAGACTACCTG  46

Qy   101 GlnValPheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
           |||||||||||||||||||||||
Db   118 CATCGAACTTGGCTGATAGGGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAAT 177

Qy    21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

Qy     1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr       20
           |||||||||||||||||||||||||||||||||||||||
Db     1 CGCCAAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAAGTTCCTAGACTACCTG  20
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Qy    41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 CACCAACTGTGCATTAAAGGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 237

RESULT 8
US-09-451-527-84/c
; Sequence 84, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
;    APPLICANT: Sim, Gek-Kee
;    APPLICANT: Yang, Shumin
;    APPLICANT: Dreitz, Matthew J.
;    APPLICANT: Wonderling, Ramani S.
;    TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;    TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;    FILE REFERENCE: IM-2-C2
;    CURRENT APPLICATION NUMBER: US/09/451,527
;    CURRENT FILING DATE: 1999-12-01
;    EARLIER APPLICATION NUMBER: 09/322,409
;    EARLIER FILING DATE: 1999-05-28
;    EARLIER APPLICATION NUMBER: 60/087,306
;    EARLIER FILING DATE: 1998-05-29
;    NUMBER OF SEQ ID NOS: 174
;    SOFTWARE: Patentin Ver. 2.0
;    SEQ ID NO 84
;    LENGTH: 402
;    TYPE: DNA
;    ORGANISM: Canis familiaris
US-09-451-527-84

Alignment Scores:
Pred. No.:                 1.43e-81       Length:          402
Score:                      610.00        Matches:         115
Percent Similarity:        100.00%        Conservative:      0
Best Local Similarity:     100.00%        Mismatches:        0
Query Match:               100.00%        Indels:            0
DB:                             4         Gaps:              0

US-10-787-382-10 (1-115) x US-09-451-527-84 (1-402)

Qy     1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr       20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  286

Qy    21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CATCGAACTTGGCTGATAGGGGGATGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAT 226

Qy    41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 CACCAACTGTGCATTAAAGGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 166

Qy    61 HisGlyGluValAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 CACGGGGAGGCTGTGGATAAAACTATTCCAAAACTTGCTTTAATAAAAGAACACATAGAG 106

Qy    81 ArgGlnLysLysSerArgCysAlaGlyLysGluArgTrpArgValThrLysPheLeuAspTyrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 CGCCAAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAAGTTCCTAGACTACCTG  46

Qy   101 GlnValPheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
           |||||||||||||||||||||||
Db   358 CAAGTATTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 402
```

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
      |||||||||||||||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 9
US-09-322-409-80
; Sequence 80, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Dreitz, Matthew J.
;   APPLICANT: Wonderling, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C1
;   CURRENT APPLICATION NUMBER: US/09/322,409
;   CURRENT FILING DATE: 1999-05-28
;   EARLIER APPLICATION NUMBER: 60/087,306
;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 154
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 80
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(430)

US-09-322-409-80

Alignment Scores:
Pred. No.:
Score: 2.71e-81
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

Length: 610
Matches: 115
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-787-382-10 (1-115) x US-09-322-409-80 (1-610)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   86 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGAACCTTGACACTGCTCCCACT 145

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   146 CATCGAACTTGGCTGATAGGCGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 205

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   206 CACCCAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
      |||||||||||||||||||||||||||||||||||||||||||||
Db   326 CGCCAAAAAAAAAAGGTGTGCAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 385

Qy   81 ArgGlnLysGlyArgCysAlaGlyValArgTrpLysPheLeuAspTyrLeu 100
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   266 CACGGGGAGGCGTGGATAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 325

Qy   61 HisGlyGluValProPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   206 CACCCAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
      |||||||||||||||||||||||||||||||||||||||||||||
Db   386 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 10
US-09-322-409-82/c
; Sequence 82, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Dreitz, Matthew J.

;   APPLICANT: Wonderling, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C1
;   CURRENT APPLICATION NUMBER: US/09/322,409
;   CURRENT FILING DATE: 1999-05-28
;   EARLIER APPLICATION NUMBER: 60/087,306
;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 154
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 82
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Canis familiaris

US-09-322-409-82

Alignment Scores:
Pred. No.:
Score: 2.71e-81
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%

Length: 610
Matches: 115
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-787-382-10 (1-115) x US-09-322-409-82 (1-610)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGAACCTTGACACTGCTCCCACT 466

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 CATCGAACTTGGCTGATAGGCGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 406

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   405 CACCCAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 346

Qy   61 HisGlyGluValProPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 CACGGGGAGGCGTGGATAAACTATTCCAAAACTGTCTTTAATAAAAGAACACATAGAG 286

Qy   81 ArgGlnLysGlyArgCysAlaGlyValArgTrpLysPheLeuAspTyrLeu 100
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285 CGCCAAAAAAAAAAGGTGTGCAGGAGAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 226

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
      |||||||||||||||||||||||||||||||||||||||||||||
Db   225 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 11
US-09-451-527-80
; Sequence 80, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Dreitz, Matthew J.
;   APPLICANT: Wonderling, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C2
;   CURRENT APPLICATION NUMBER: US/09/451,527
;   CURRENT FILING DATE: 1999-12-01
;   EARLIER APPLICATION NUMBER: 09/322,409
;   EARLIER FILING DATE: 1999-05-28
;   EARLIER APPLICATION NUMBER: 60/087,306
;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 80
;   LENGTH: 610
;   TYPE: DNA

```
; ORGANISM: Canis familiaris
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)...(430)
US-09-451-527-80

Alignment Scores:
Pred. No.:
Score:                  2.71e-81      Length:         610
Percent Similarity:     100.00%       Matches:        115
                                      Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            4             Indels:         0
DB:                                   Gaps:           0

US-10-787-382-10 (1-115) x US-09-451-527-80 (1-610)

Qy    1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   86 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACT 145

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  146 CATCGAACTTGGCTGATAGGCGGGGAACCTGATGATTCCTACTCCCTGAAAATAAAAT 205

Qy   41 HisGlnLeuCysIleLysGlyValValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  206 CACCAACTGTGCATTAAAAGAAGGTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 265

Qy   61 HisGlyGluAlaValAlaSerProLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  266 CACGGGCGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 325

Qy   81 ArgGlnLysLysArgCysAlaGlyGlyLeuArgTrpAspValThrLysPheLeuAspTyrLeu 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  326 CGCCAAAAAAAAAGGTGTGCAGGAGAAGATGGACGAGTGACAAAGTTCCTAGACTACCTG 385

Qy  101 GlnValPheLeuGlyValIleIleAsnThrGluTrpProThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  386 CAAGTATTTCTTGGTGTAATAAACACCGGAGTGGACACCGGAAAGT 430


RESULT 12
US-09-451-527-82/c
; Sequence 82, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shunin
;   APPLICANT: Dreitz, Matthew J.
;   APPLICANT: Wondering, Ramani S.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C2
;   CURRENT APPLICATION NUMBER: US/09/451,527
;   CURRENT FILING DATE: 1999-12-01
;   EARLIER APPLICATION NUMBER: 09/322,409
;   EARLIER FILING DATE: 1999-05-28
;   EARLIER APPLICATION NUMBER: 60/087,306
;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-451-527-82

Alignment Scores:
Pred. No.:
Score:                  2.71e-81      Length:         610
Percent Similarity:     100.00%       Matches:        115
                                      Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            4             Indels:         0
DB:                                   Gaps:           0

US-10-787-382-10 (1-115) x US-09-451-527-82 (1-610)

Qy    1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  525 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACT 466

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  465 CATCGAACTTGGCTGATAGGCGGGGAACCTGATGATTCCTACTCCCTGAAAATAAAAT 406

Qy   41 HisGlnLeuCysIleLysGlyValValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  405 CACCAACTGTGCATTAAAAGAAGGTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 346

Qy   61 HisGlyGluAlaValAlaSerProLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  345 CACGGGCGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 286

Qy   81 ArgGlnLysLysArgCysAlaGlyGlyLeuArgTrpAspValThrLysPheLeuAspTyrLeu 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  285 CGCCAAAAAAAAAGGTGTGCAGGAGAAGATGGACGAGTGACAAAGTTCCTAGACTACCTG 226

Qy  101 GlnValPheLeuGlyValIleIleAsnThrGluTrpProThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  225 CAAGTATTTCTTGGTGTAATAAACACCGGAGTGGACACCGGAAAGT 181


RESULT 13
US-09-371-615A-1
; Sequence 1, Application US/0937161615A
; Patent No. 6537781
; GENERAL INFORMATION:
;   APPLICANT: IDEXX LABORATORIES
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
;   TITLE OF INVENTION: CANINE INTERLEUKIN 5
;   FILE REFERENCE: 03604001700US00
;   CURRENT APPLICATION NUMBER: US/09/371,615A
;   CURRENT FILING DATE: 1999-08-10
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 405
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-371-615A-1

Alignment Scores:
Pred. No.:
Score:                  3.19e-80      Length:         405
Percent Similarity:     99.13%        Matches:        114
                                      Conservative:   0
Best Local Similarity:  99.13%        Mismatches:     1
Query Match:            98.52%        Indels:         0
DB:                                   Gaps:           0

US-10-787-382-10 (1-115) x US-09-371-615A-1 (1-405)

Qy    1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  525 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACT 117

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  118 CATCGAACTTGGCTGATAGGCGGGGAACCTGATGATTCCTACTCCCTGAAAATAAAAT 177

Qy   41 HisGlnLeuCysIleLysGlyValValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 CACCAACTGTGCATTAAAAGAAGGTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC 237

Qy   61 HisGlyGluAlaValAlaSerProLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 CACGGGCGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 297

Qy   81 ArgGlnLysLysArgCysAlaGlyGlyLeuArgTrpAspValThrLysPheLeuAspTyrLeu 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  298 CGCCAAAAAAAAAGGTGTGCAGGAGAAGATGGACGAGTGACAAAGTTCCTAGACTACCTG 100
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Db    298  CGCCAAAAAAAAGGTGTGCAGGAGGAGAGATGGAGAGGAGGTGACAAAGTTCCTAGACTACCTG 357
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Qy    101  GlnValPheLeuGlyValIleAsnThrGluThrTrpThrProGluSer 115

Db    358  CAAGTATTTCTTGGTGTAATAAACACCGAGTCGACAATGGAAAGT 402
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RESULT 14
US-09-079-839-2
; Sequence 2, Application US/09079839
; Patent No. 6048726
; GENERAL INFORMATION:
;   APPLICANT: Weltman, Joel K.
;   APPLICANT: Karim, Aftab S.
;   TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION
;   FILE REFERENCE: 09998/002001
;   CURRENT APPLICATION NUMBER: US/09/079,839
;   CURRENT FILING DATE: 1998-05-15
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 816
;   TYPE: DNA
;   ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:
Score: 3.64e-43
Percent Similarity: 356.00
Best Local Similarity: 76.79%
Query Match: 62.50%
DB: 58.36%
                            3

                            Length: 816
                            Matches: 70
                            Conservative: 16
                            Mismatches: 26
                            Indels: 0
                            Gaps: 0

US-10-787-382-10 (1-115) x US-09-079-839-2 (1-816)

Qy   4   GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
           ||| ::: || |||| || ::
Db   111 GAAATTCCCACAAGTGCCATTGGTGAAAGACTTGGCACTGCTTTCTTACTCATCGAACT 170

Qy   24   TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
           |||| ::: || || :::
Db   171 CTGCTGATAGGCCAATGGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAAATCACCAACTG 230

Qy   44   CysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
           || ||| ::: ||||| ||||| ||||||
Db   231 TGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAAACTGTGCAAGGGGGT 290

Qy   64   AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
           |||||| ::: || :::: || :::   :::
Db   291 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATAACATTGACGGCCAAAA 350

Qy   84   LysArgCysAlaGlyGlyArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
           || ::: ||| ::: ||||||||||| |||
Db   351 AAAAAGTGTGGAGAAGAACGACGGAGGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 410

Qy   104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
           ||||||||||| ::: ||||||||||||||||
Db   411 CTTGGTGTAATGAACACCGAGTGGATAATAGAAAGT 446
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RESULT 15
US-09-180-864-1
; Sequence 1, Application US/09180864
; Patent No. 6465616
; GENERAL INFORMATION:
;   APPLICANT: Lopez, Angel
;   APPLICANT: Vadas, Matthew
;   APPLICANT: Shannon, Frances
;   APPLICANT: Bagiras, Stan
;   APPLICANT: Hey, Allan W
;   TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
;   FILE REFERENCE: 9922Z
;   CURRENT APPLICATION NUMBER: US/09/180,864

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; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 08/591,438
; PRIOR FILING DATE: 1994-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 377
;   TYPE: DNA
;   ORGANISM: nucleotide sequence encoding modified IL-5
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(366)
US-09-180-864-1

Alignment Scores:
Pred. No.:
Score:                      6.22e-43
Percent Similarity:         351.00
Best Local Similarity:      75.89%
Query Match:                61.61%
DB:                         57.54%
                            3

                            Length:       377
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                            Conservative: 16
                            Mismatches:   27
                            Indels:       0
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US-10-787-382-10 (1-115) x US-09-180-864-1 (1-377)

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Qy    4    GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
           |||                ::: ||               ||||  ||     ::
Db    31   GAAATTCCCACAAGTGCATTGGTGAAACGTACCTTGGCACTGCTTTCTTACTCATCGAACT 90

Qy    24   TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
           ||||                  :::  ||              ||   :::
Db    91   CTGCTGATAGGCCAATGGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAAATCACCAACTG 150

Qy    44   CysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
           ||  |||         :::  |||||          |||||      ||||||
Db    151  TGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAAACTGTGCAAGGGGGT 210

Qy    64   AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
           ||||||    ::: ||    ::::              ||     :::   :::
Db    211  ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATAACATTGACGGCCAAAA 270

Qy    84   LysArgCysAlaGlyGlyArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
           ||  :::         |||                ::: |||||||||||      |||
Db    271  AAGAAGTGTGGAGAAGAACGTCGTCGTGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 330

Qy    104  LeuGlyValIleAsnThrGluTrpThrProGluSer 115
           |||||||||||    ::: ||||||||||||||||
Db    331  CTTGGTGTAATGAACACCGAGTGGATCATCGAATCC 366
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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: August 6, 2005, 22:43:11 ; Search time 477.55 Seconds
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Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVAEFLTLLIST..........FLDYLQVFLGVINTEWTPES 115

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	610	100.0	345	9	US-09-755-633-9	Sequence 9, Appli
2	610	100.0	345	9	US-09-755-633-11	Sequence 11, Appl
3	610	100.0	345	14	US-10-218-654-85	Sequence 85, Appl
4	610	100.0	345	14	US-10-218-654-87	Sequence 87, Appl
5	610	100.0	345	15	US-10-262-439-85	Sequence 85, Appl
6	610	100.0	345	15	US-10-262-439-87	Sequence 87, Appl
7	610	100.0	345	19	US-10-787-382-9	Sequence 9, Appl1
8	610	100.0	402	19	US-10-262-439-84	Sequence 84, Appl
9	610	100.0	402	9	US-09-755-633-7	Sequence 7, Appli
10	610	100.0	402	9	US-09-755-633-8	Sequence 8, Appli
11	610	100.0	402	14	US-10-218-654-83	Sequence 83, Appl
12	610	100.0	402	14	US-10-218-654-84	Sequence 84, Appl
13	610	100.0	402	15	US-10-262-439-83	Sequence 83, Appl
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15	610	100.0	402	19	US-10-787-382-8	Sequence 8, Appli
16	610	100.0	402	9	US-09-755-633-6	Sequence 6, Appli
17	610	100.0	610	19	US-10-787-382-7	Sequence 7, Appli
18	610	100.0	610	14	US-10-218-654-80	Sequence 80, Appl
19	610	100.0	610	14	US-10-218-654-82	Sequence 82, Appl
20	610	100.0	610	15	US-10-262-439-80	Sequence 80, Appl
21	610	100.0	610	15	US-10-262-439-82	Sequence 82, Appl
22	610	100.0	610	19	US-10-262-439-82	Sequence 82, Appl
23	610	100.0	610	19	US-10-787-382-4	Sequence 4, Appli
24	610	100.0	610	9	US-10-787-382-6	Sequence 6, Appli
25	546.5	89.6	671	9	US-09-755-633-21	Sequence 21, Appl
26	546.5	89.6	671	19	US-10-787-382-21	Sequence 21, Appl
27	363	59.5	1658	19	US-10-787-382-19	Sequence 19, Appl
28	363	59.5	1658	9	US-09-755-633-19	Sequence 19, Appl
29	362.5	59.4	1658	19	US-10-787-382-18	Sequence 18, Appl
30	362.5	59.4	1658	9	US-09-755-633-18	Sequence 18, Appl
31	357	58.5	864	16	US-10-295-074-12	Sequence 12, Appl
32	357	58.5	864	20	US-10-846-911-12	Sequence 12, Appl
33	357	58.5	459	22	US-10-880-101A-85	Sequence 85, Appl
34	356	58.4	459	17	US-10-191-997-90	Sequence 90, Appl
35	356	58.4	816	21	US-10-929-182-4	Sequence 4, Appli
36	356	58.4	816	22	US-10-880-101A-87	Sequence 87, Appl
37	356	58.4	858	16	US-10-295-074-8	Sequence 8, Appli
38	356	58.4	858	16	US-10-295-074-10	Sequence 10, Appl
39	356	58.4	858	20	US-10-846-911-8	Sequence 8, Appli
40	356	58.4	864	20	US-10-846-911-10	Sequence 10, Appl
41	356	58.4	864	16	US-10-295-074-14	Sequence 14, Appl
42	356	58.4	864	20	US-10-846-911-14	Sequence 14, Appl
43	350	57.4	816	18	US-10-641-643-1236	Sequence 1236, Ap
44	228.5	37.5	3241	22	US-10-880-101A-91	Sequence 91, Ap
45	222	36.4	6727	9	US-09-800-629A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-755-633-9
Sequence 9, Application US/09755633
Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306

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;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn Ver. 2.1
;
;   SEQ ID NO 9
;   TYPE: DNA
;   LENGTH: 345
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(345)
US-09-755-633-9

Alignment Scores:
Pred. No.:
Score:                      4.78e-78
Percent Similarity:         610.00        Length:          345
Best Local Similarity:      100.00%       Matches:         115
Query Match:                100.00%       Conservative:    0
DB:                         9             Mismatches:      0
                                          Indels:          0
                                          Gaps:            0

US-10-787-382-10 (1-115) x US-09-755-633-9 (1-345)

Qy   1    PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr      20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1    TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTGACACTGCTCTCCACT     60

Qy   21   HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn     40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   CATCGAACTTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT    120

Qy   41   HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC    180

Qy   61   HisGlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu    80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CACGGGGAGGCTGTGGCTGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG    240

Qy   81   ArgGlnLysAlaGlyGluArgCysAlaGlyTyrTrpArgValThrArgValThrLysPheTyrLeu  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CGCCAAAAAGCAGGGGAGCGGTGTGCAGGGTACTGGAGAGTGACAAAAGTTCCTAGACTACCTG   300

Qy   101  GlnValPheLeuGlyValIleAsnThrGluTrpProThrProGluSer                   115
          |||||||||||||||||||||||||||||||
Db   301  CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCGGAAAGT                    345
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;   Score:                       610.00        Matches:         115
;   Percent Similarity:          100.00%       Conservative:    0
;   Best Local Similarity:       100.00%       Mismatches:      0
;   Query Match:                 100.00%       Indels:          0
;   DB:                          9             Gaps:            0

US-10-787-382-10 (1-115) x US-09-755-633-11 (1-345)

Qy   1    PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr         20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCCTGACACTGCTCTCCACT     286

Qy   21   HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn     40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  CATCGAACTTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT    226

Qy   41   HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC    166

Qy   61   HisGlyGluAlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu    80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165  CACGGGGAGGCTGTGGCTGATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG    106

Qy   81   ArgGlnLysAlaGlyGluArgCysAlaGlyTyrTrpArgValThrArgValThrLysPheTyrLeu  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105  CGCCAAAAAGCAGGGGAGCGGTGTGCAGGGTACTGGAGAGTGACAAAAGTTCCTAGACTACCTG   46

Qy   101  GlnValPheLeuGlyValIleAsnThrGluTrpProThrProGluSer                   115
          |||||||||||||||||||||||||||||||
Db   45   CAAGTATTTCTTGGTGTAATAAACACCGAGTGGGACACCGGAAAGT                    1
```

```
RESULT 3
US-10-218-654-85
;   Sequence 85, Application US/10218654
;   Publication No. US20030099609A1
;   GENERAL INFORMATION:
;   APPLICANT: Sim, Gek-Kee
;   APPLICANT: Yang, Shumin
;   APPLICANT: Wonderling, Ramani S.
;   APPLICANT: Dreitz, Matthew J.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C1
;   CURRENT APPLICATION NUMBER: US/10/218,654
;   CURRENT FILING DATE: 2002-08-13
;   PRIOR APPLICATION NUMBER: US/09/322,409
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 60/087,306
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 154
;   SOFTWARE: PatentIn Ver. 2.0
;
;   SEQ ID NO 85
;   TYPE: DNA
;   LENGTH: 345
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(345)
US-10-218-654-85

Alignment Scores:
Pred. No.:
Score:                      4.78e-78
Percent Similarity:         610.00        Length:          345
Best Local Similarity:      100.00%       Matches:         115
Query Match:                100.00%       Conservative:    0
DB:                         14            Mismatches:      0
                                          Indels:          0
                                          Gaps:            0

US-10-787-382-10 (1-115) x US-10-218-654-85 (1-345)

Qy   1    PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr         20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 2
US-09-755-633-11/c
;   Sequence 11, Application US/0975563
;   Patent No. US20020127200A1
;   GENERAL INFORMATION:
;   APPLICANT: Yang, Shumin
;   APPLICANT: McCall, Catherine A.
;   APPLICANT: Weber, Eric R.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C1-C1
;   CURRENT APPLICATION NUMBER: US/09/755,633
;   CURRENT FILING DATE: 2001-01-05
;   PRIOR APPLICATION NUMBER: 09/322,409
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 60/087,306
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn Ver. 2.1
;
;   SEQ ID NO 11
;   TYPE: DNA
;   LENGTH: 345
;   ORGANISM: Canis familiaris
US-09-755-633-11

Alignment Scores:
Pred. No.:                  4.78e-78      Length:          345
```

RESULT 4

US-10-218-654-87/c

Sequence 87, Application US/10218654

Publication No. US20030095609A1

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C1

CURRENT APPLICATION NUMBER: US/10/218,654

CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: US/09/322,409

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/087,306

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 154

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 87

LENGTH: 345

TYPE: DNA

ORGANISM: Canis familiaris

US-10-218-654-87

Alignment Scores:

Pred. No.:	
Score:	4.78e-78
Percent Similarity:	610.00
Best Local Similarity:	100.00%
Query Match:	100.00%

Length:		345
Matches:		115
Conservative:		0
Mismatches:		0
Indels:		0
Gaps:		0

DB:

US-10-787-382-10 (1-115) x US-10-218-654-87 (1-345)

```
Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnMetIleProThrProGluSerLysAsn  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATCTTCTACTCCTGAAAAATAAAAT 226

Qy     41 HisArgLeuLysLysArgCysAlaGlyValThrArgValThrLysPheLeuAspTyrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CACCAACTGTGCATTAAAGAAGTTTTTCAGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy     61 HisGlyGluValAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGlu  80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACGGGGGAGGCTGTGGAATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy    101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
            |||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAAGTATTTCTTGGGTGTAATAAACACCGGAGTGGACACCGGAAAGT 345
```

RESULT 5

US-10-262-439-85

Sequence 85, Application US/10262439

Publication No. US20030143196A1

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C2

CURRENT APPLICATION NUMBER: US/10/262,439

CURRENT FILING DATE: 2002-09-30

PRIOR APPLICATION NUMBER: US/09/451,527

PRIOR FILING DATE: 1999-12-01

PRIOR APPLICATION NUMBER: 09/322,409

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/087,306

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 174

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 85

LENGTH: 345

TYPE: DNA

ORGANISM: Canis familiaris

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(345)

US-10-262-439-85

Alignment Scores:

Pred. No.:	
Score:	4.78e-78
Percent Similarity:	610.00
Best Local Similarity:	100.00%
Query Match:	100.00%

Length:		345
Matches:		115
Conservative:		0
Mismatches:		0
Indels:		0
Gaps:		0

DB:

US-10-787-382-10 (1-115) x US-10-262-439-85 (1-345)

```
Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  46

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnMetIleProThrProGluSerLysAsn  40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     45 CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATCTTCTACTCCTGAAAAATAAAAT 120

Qy     41 HisArgLeuLysLysArgCysAlaGlyValThrArgValThrLysPheLeuAspTyrLeu 100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGTATAGACACATTGAAGAACCAAACTGCC 180

Qy     61 HisGlyGluValAlaValAlaAspLysPheGlnAsnLeuSerLeuIleLysGluHisIleGlu  80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CACGGGGGAGGCTGTGGAATAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 240

Qy    101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
            |||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAAGTATTTCTTGGGTGTAATAAACACCGGAGTGGACACCGGAAAGT 345
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RESULT 6
US-10-262-439-87/C
; Sequence 87, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-87

Alignment Scores:
Pred. No.:
Score: 4.78e-78   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 15   Indels: 0
                                       Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-87 (1-345)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr   20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy   21 HisArgThrTrpLeuIleGlyIleTyrIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsn   40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 285 CATCGAACTTGGCTGATAGGCGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrArgLeuLysAsnGlnThrAla   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 225 CACCAACTGTGCATTAAAGAAGTTTTTCAGGTATAGACACATTGAAGAACCAAAACTGCC 166

Qy   61 HisGlyGluAlaValAspPheLysArgValThrArgPheLeuAspTyrLeu   80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 165 CACGGCGGAGGCTGTCGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysLysArgGlyAlaGlyGlyLysArgTrpArgValThrArgPheLeuAspTyrLeu 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 105 CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG   46

Qy 101 GlnValPheLeuGlyValValIleAsnThrGluTrpThrProGluSer 115
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT   1

RESULT 7
US-10-787-382-9
; Sequence 9, Application US/10787382
; Publication NO. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-10-787-382-9

Alignment Scores:
Pred. No.:
Score: 4.78e-78   Length: 345
Percent Similarity: 610.00   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 19   Indels: 0
                                       Gaps: 0

US-10-787-382-10 (1-115) x US-10-787-382-9 (1-345)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr   20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT   60

Qy   21 HisArgThrTrpLeuIleGlyIleTyrIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsn   40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGAACTTGGCTGATAGGCGGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT 120

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleIleAspThrArgLeuLysAsnGlnThrAla   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGTATAGACACATTGAAGAACCAAAACTGCC 180

Qy   61 HisGlyGluAlaValAspPheLysArgValThrArgPheLeuAspTyrLeu   80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CACGGCGGAGGCTGTCGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 240

Qy   81 ArgGlnLysLysArgGlyAlaGlyGlyLysArgTrpArgValThrArgPheLeuAspTyrLeu 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300

Qy 101 GlnValPheLeuGlyValValIleAsnThrGluTrpThrProGluSer 115
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 345

RESULT 8
US-10-787-382-11/c
; Sequence 11, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; CURRENT APPLICATION NUMBER: IM-2-C1
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/10/787,382
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29

```
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 11
;   LENGTH: 345
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-10-787-382-11

Alignment Scores:
Pred. No.:
Score:                  4.78e-78      Length:        345
Percent Similarity:     610.00        Matches:       115
Best Local Similarity:  100.00%       Conservative:  0
Query Match:            100.00%       Mismatches:    0
DB:                     19            Indels:        0
                                      Gaps:          0

US-10-787-382-10 (1-115) x US-10-787-382-11 (1-345)

Qy     1  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr    20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  286

Qy    21  HisArgThrTrpLeuIleGlyIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT  226

Qy    41  HisGlnLeuCysIleLeuLysGluValPheGlnGlyIleAspIleLeuAspThrLeuLeuLysGluAsnGlnThrAla  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC  166

Qy    61  HisGlyGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluGlu  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165  CACGGGGGAGGCTGTGATAAAACTATTCCAAAAACTGTCTTAATAAAAGAACACATTGAG  106

Qy    81  ArgGlnLysGlyArgCysAlaGlyGluArgTrpProArgValThrArgValThrLysPheLeuAspTyrLeu  100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105  CGCCAAAAAAAAGGTGTGCAGGAGAGAGAGATGGAGTGACAAAGTTCCTAGAGACTACCTG   46

Qy   101  GlnValPheLeuGlyValValIleAsnThrGluTrpThrProGluSer  115
          |||||||||||||||||||||||||||||||||||||||||||||
Db    45  CAAGTATTTCTTGGTGTTAATAAACACCGAGTGGACACCGGAAAGT    1
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```
RESULT 9
US-09-755-633-7
;   Sequence 7, Application US/09755633
;   Patent No. US20020127200A1
;   GENERAL INFORMATION:
;   APPLICANT: Yang, Shumin
;   APPLICANT: McCall, Catherine A.
;   APPLICANT: Weber, Eric R.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C1-C1
;   CURRENT APPLICATION NUMBER: US/09/755,633
;   CURRENT FILING DATE: 2001-01-05
;   PRIOR APPLICATION NUMBER: 09/322,409
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 60/087,306
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 7
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-755-633-7

Alignment Scores:
Pred. No.:
Score:                  5.99e-78      Length:        402
Percent Similarity:     610.00        Matches:       115
Best Local Similarity:  100.00%       Conservative:  0
Query Match:            100.00%       Mismatches:    0
DB:                     9             Indels:        0
                                      Gaps:          0

US-10-787-382-10 (1-115) x US-09-755-633-7 (1-402)

Qy     1  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr    20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    58  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  117

Qy    21  HisArgThrTrpLeuIleGlyIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118  CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT  177

Qy    41  HisGlnLeuCysIleLeuLysGluValPheGlnGlyIleAspIleLeuAspThrLeuLeuLysGluAsnGlnThrAla  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178  CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAAACTGCC  237

Qy    61  HisGlyGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLeuLysGluGlu  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238  CACGGGGGAGGCTGTGATAAAACTATTCCAAAAACTGTCTTTAATAAAAGAACACATTGAG  297

Qy    81  ArgGlnLysGlyArgCysAlaGlyGluArgTrpProArgValThrArgValThrLysPheLeuAspTyrLeu  100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298  CGCCAAAAAAAAGGTGTGCAGGAGAGAGAGATGGAGTGACAAAGTTCCTAGAGACTACCTG  357

Qy   101  GlnValPheLeuGlyValValIleAsnThrGluTrpThrProGluSer  115
          |||||||||||||||||||||||||||||||||||||||||||||
Db   358  CAAGTATTTCTTGGTGTTAATAAACACCGAGTGGACACCGGAAAGT  402
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RESULT 10
US-09-755-633-8/c
;   Sequence 8, Application US/09755633
;   Patent No. US20020127200A1
;   GENERAL INFORMATION:
;   APPLICANT: Yang, Shumin
;   APPLICANT: McCall, Catherine A.
;   APPLICANT: Weber, Eric R.
;   TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
;   FILE REFERENCE: IM-2-C1-C1
;   CURRENT APPLICATION NUMBER: US/09/755,633
;   CURRENT FILING DATE: 2001-01-05
;   PRIOR APPLICATION NUMBER: 09/322,409
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 60/087,306
;   PRIOR FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 8
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-755-633-8

Alignment Scores:
Pred. No.:
Score:                  5.99e-78      Length:        402
Percent Similarity:     610.00        Matches:       115
Best Local Similarity:  100.00%       Conservative:  0
Query Match:            100.00%       Mismatches:    0
DB:                     9             Indels:        0
                                      Gaps:          0

US-10-787-382-10 (1-115) x US-09-755-633-8 (1-402)

Qy     1  PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr    20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT  286

Qy    21  HisArgThrTrpLeuIleGlyIleAspGlyAsnLeuMetIleProThrProGluAsnLysAsn  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  CATCGAACTTGGCTGATAGGCGGATGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAT  226

Qy    41  HisGlnLeuCysIleLeuLysGluValPheGlnGlyIleAspIleLeuAspThrLeuLeuLysGluAsnGlnThrAla  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 11
US-10-218-654-83

; Sequence 83, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-83

Alignment Scores:
Pred. No.:
Score: 5.99e-78
Percent Similarity: 610.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 14

Length: 402
Matches: 115
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-787-382-10 (1-115) x US-10-218-654-83 (1-402)

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Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCTCCACT 58

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 CATCGAACTTGGCTGATAGGCGGGGACCCTGATGATTCCTACTCCTGAAAATAAAAAT 118

Qy     41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrThrLeuLysAsnGlnThrAla 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CATCGAACTTGGCTGATAGGCGGGAACCTGATGATTCCTACTCCTGAAAATAAAAAAT 177

Qy    101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
            |||||||||||||||||||||||||||||||||||||||||||
Db    178 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAGACCAAACTGCC 237
```

Qy   41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrThrLeuLysAsnGlnThrAla 60

Db   105 CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGACAAAGTTCCTAGACTACCTG 46

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
Db   118 CATCGAACTTGGCTGATAGGCGGGGACCCTGATGATTCCTACTCCTGAAAATAAAAAT 177

Qy   81 ArgGlnLysLysArgCysAlaGlyGluArgAspValThrArgValThrLysPheLeuAspTyrLeu 100
Db   165 CACGGGGGAGGCTGTGGATAAACTATTCCAAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   61 HisGlyGluValAspLysIleProPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
Db   105 CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGACAAAGTTCCTAGACTACCTG 46

Qy   101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
Db   45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

Db   225 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAGACCAAACTGCC 166

RESULT 12
US-10-218-654-84/c

; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Alignment Scores:
Pred. No.:
Score: 5.99e-78
Percent Similarity: 610.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 14

Length: 402
Matches: 115
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-787-382-10 (1-115) x US-10-218-654-84 (1-402)

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Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCTCCACT 286

Qy     21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 CATCGAACTTGGCTGATAGGCGGGGACCCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy     41 HisGlnLeuCysIleLysGluValPheGlnGlyIleAspThrThrLeuLysAsnGlnThrAla 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAGACCAAACTGCC 166

Qy     61 HisGlyGluValAspLysIleProPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACGGGGGAGGCTGTGGATAAACTATTCCAAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy     81 ArgGlnLysLysArgCysAlaGlyGluArgAspValThrArgValThrLysPheLeuAspTyrLeu 100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGACAAAGTTCCTAGACTACCTG 46

Qy    101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
            |||||||||||||||||||||||||||||||||||||||||||
Db     45 CAAGTATTTCTTGGGTGTAATAAACACCGAGTGGACACCGGAAAGT 1
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RESULT 13
US-10-262-439-83

; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2

CURRENT APPLICATION NUMBER: US/10/262,439
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/451,527
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 83
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris

US-10-262-439-83

Alignment Scores:
Pred. No.:
Score: 610.00   Length: 402
Percent Similarity: 100.00%   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 15   Mismatches: 0
                            5.99e-78   Indels: 0
                                            Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-83 (1-402)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTTGGCAGAGAACCTTGACACTGTCTCCACT 58

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 CATCGAACTTGGCTGATAGGCGATGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAAT 117

Qy   41 HisGlnLeuCysIleIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118 CACCAACTGTGCATTAAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAAACCAAAACTGCC 177

Qy   61 HisGlyGluAlaValAlaAspLysAlaArgTrpGlnAsnLeuSerLeuIleLeuLysGluHisIleLeuGlu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 CACGGGGAGGCTGTGGATAAAGCTATTCCAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 237

Qy   81 ArgGlnLysArgCysAlaAlaGlyLeuArgTrpArgValThrLysPheLeuAspTyrLeu 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 CGCCAAAAAAAAAAGGTGTGCAGGAGAGATGGAGAAAGATCGAGAGAGTTCCTAGACTACCTG 297

Qy 101 GlnValPheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
         |||||||||||||||||||||||||||||||||||||||||||||
Db 298 CAAGTATTTCTTGGGTGTAATAAACACCCGAGTGGACACCGGAAAGT 358

RESULT 14
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84

LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris

US-10-262-439-84

Alignment Scores:
Pred. No.:
Score: 610.00   Length: 402
Percent Similarity: 100.00%   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 15   Mismatches: 0
                            5.99e-78   Indels: 0
                                            Gaps: 0

US-10-787-382-10 (1-115) x US-10-262-439-84 (1-402)

Qy   1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThr 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTTGGCAGAGAACCTTGACACTGTCTCCACT 286

Qy   21 HisArgThrTrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 285 CATCGAACTTGGCTGATAGGCGATGGGAAACCTGATGATTCCTACTCCTGAAAATAAAAAT 226

Qy   41 HisGlnLeuCysIleIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 225 CACCAACTGTGCATTAAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAAACCAAAACTGCC 166

Qy   61 HisGlyGluAlaValAlaAspLysAlaArgTrpGlnAsnLeuSerLeuIleLeuLysGluHisIleLeuGlu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 165 CACGGGGAGGCTGTGGATAAAGCTATTCCAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 106

Qy   81 ArgGlnLysArgCysAlaAlaGlyLeuArgTrpArgValThrLysPheLeuAspTyrLeu 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 105 CGCCAAAAAAAAAAGGTGTGCAGGAGAGATGGAGAAAGATCGAGAGAGTTCCTAGACTACCTG 46

Qy 101 GlnValPheLeuGlyValIleLeuAsnThrGluTrpThrProGluSer 115
         |||||||||||||||||||||||||||||||||||||||||||||
Db   45 CAAGTATTTCTTGGGTGTAATAAACACCCGAGTGGACACCGGAAAGT 1

RESULT 15
US-10-787-382-7
; Sequence 7, Application US/10787382
; Publication No. US20040191868A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;   ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/787,382
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7

LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris

US-10-787-382-7

Alignment Scores:
Pred. No.:
Score: 610.00   Length: 402
Percent Similarity: 100.00%   Matches: 115
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 19   Mismatches: 0
                            5.99e-78   Indels: 0
                                            Gaps: 0

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US-10-787-382-10 (1-115) x US-10-787-382-7 (1-402)

Qy      1 PheAlaValGluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThr 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 TTTGCTGTAGAAAATCCAATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACT 117

Qy     21 HisArgThrTrpLeuIleGlyIleGlyAsnLeuMetIleProThrProGluAsnLysAsn 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CATCGAACTTGGCTGATAGGCCGATGGGAACCTGATGATTCCTACTCCCTGAAAATAAAAAT 177

Qy     41 HisGlnLeuCysIleLysGlyValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237

Qy     61 HisGlyGluAlaValAspLysLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CACGGGGAGGCTGTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAGAACACATTAGAG 297

Qy     81 ArgGlnLysLysArgCysAlaGlyIleGlyArgTrpArgValThrLysPheLeuAspTyrLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 CGCCAAAAAAAAAGGTGTGCAGGAGGAATGGGAGAGTGACAAAGTTCCTAGACTACCTG 357

Qy    101 GlnValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    358 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCCGAAAGT 402
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Search completed: August 7, 2005, 03:16:01
Job time : 479.55 secs

OM protein - nucleic search, using frame_plus_p2n model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             August  6, 2005, 19:45:30 ; Search time 2415 Seconds
                                              (without alignments)
                                              1812.584 Million cell updates/sec

Title:              US-10-787-382-10
Perfect score:      610
Sequence:           1 FAVENPMNRLVAETLTLLST..........FLDYLQVFLGVINTEWTPES 115

Scoring table:      BLOSUM62
                    Xgapop   10.0 ;  Xgapext   0.5
                    Ygapop   10.0 ;  Ygapext   0.5
                    Pgapop    6.0 ;  Pgapext   7.0
                    Delop     6.0 ,  Delext    7.0

Searched:           34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:        68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

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 -DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTPFMT=pto -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
 -USER=US10787382 @CGN 1 1 6628 @runat_04082005_084752_19305 -NCPU=6 -ICPU=3
 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
             1: gb_est1:*
             2: gb_est2:*
             3: gb_htc:*
             4: gb_est3:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_gss1:*
             9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	356.5	58.4	622	9	CE331159	CE331159 tigr-gss-
2	356	58.4	405	9	AY412020	AY412020 Homo sapi
3	356	58.4	405	9	CD559532	CD559532 AGENCOURT
4	356	58.4	456	6	CD559686	CD559686 AGENCOURT
5	356	58.4	470	6	CD559687	CD559687 AGENCOURT
6	356	58.4	492	6	CD559533	CD559533 AGENCOURT
7	343	56.2	458	3	BC066279	BC066279 Homo sapi
8	343	56.2	458	3	BC066280	BC066280 Homo sapi
9	343	56.2	463	6	CD559535	CD559535 AGENCOURT

c	10	343	56.2	467	6	CD559690	CD559690 AGENCOURT
c	11	343	56.2	473	6	CD559689	CD559689 AGENCOURT
c	12	343	56.2	489	6	CD559536	CD559536 AGENCOURT
c	13	343	56.2	817	3	BC069137	BC069137 Homo sapi
c	14	337	55.2	405	9	AY412021	AY412021 Pan trogl
c	15	332	54.4	456	3	BC066281	BC066281 Homo sapi
c	16	332	54.4	467	6	CD559688	CD559688 AGENCOURT
c	17	332	54.4	478	6	CD559534	CD559534 AGENCOURT
c	18	324	53.1	477	6	CD559608	CD559608 AGENCOURT
c	19	307	50.3	399	9	AY412022	AY412022 Mus muscu
c	20	186	30.5	781	9	CR235404	CR235404 Reverse B
c	21	165	27.0	503	5	BQ598873	BQ598873 MI-P-B4-a
c	22	86	14.1	811	4	BI247887	BI247887 602959820
c	23	82.5	13.5	412	5	BW573727	BW573727 BW573727.
c	24	81	13.3	496	1	AA689677	AA689677 vss03c02.r
c	25	81	13.3	1267	5	CR727373	CR727373 Tetraodon
c	26	80.5	13.2	518	4	BM284184	BM284184 ki3lb02.y
c	27	80.5	13.2	589	6	CD305286	CD305286 StrPu691.
c	28	79.5	13.0	618	2	BE920538	BE920538 EST424307
c	29	79.5	13.0	675	4	BI561257	BI561257 603256408
c	30	79	13.0	425	2	AW068198	AW068198 cn23c07.y
c	31	79	13.0	504	5	CR047608	CR047608 NISC_gg03
c	32	79	13.0	606	7	CO896018	CO896018 BovGen_24
c	33	79	13.0	607	5	BQ018244	BQ018244 UI-H-DH1-
c	34	79	13.0	644	5	CR047607	CR047607 NISC_gg03
c	35	79	13.0	660	7	CN371286	CN371286 170060000
c	36	79	13.0	666	7	CN371286	CN371286 UI-CP-FNO
c	37	79	13.0	721	7	CA311187	CA311187 UI-H-EU0-
c	38	79	13.0	728	6	CN480217	CN480217 UI-H-EU0-
c	39	79	13.0	728	7	CA314164	CA314164 UI-CF-FNO
c	40	79	13.0	736	5	CN371285	CN371285 170004245
c	41	79	13.0	756	4	AW068198	AW068198 UI-H-FH1-
c	42	79	13.0	759	8	BG389597	BG389597 60241A324
c	43	79	13.0	781	8	BZ542697	BZ542697 OGAH0967C
c	44	79	13.0	812	5	BU933793	BU933793 AGENCOURT
c	45	79	13.0	904	4	BM462936	BM462936 AGENCOURT
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ALIGNMENTS

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RESULT 1
CE331159
LOCUS       CE331159                 622 bp    DNA     linear   GSS 26-SEP-2003
DEFINITION  tigr-gss-dog-170003339985568 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE331159
VERSION     CE331159.1  GI:36147469
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
  MEDLINE   22875432
   PUBMED   14512627
  COMMENT   Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirkness@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1..622
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
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ORIGIN

/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

Alignment Scores:

Pred. No.:   2.32e-35
Score: 356.50
Percent Similarity: 65.22%   Matches: 75
Best Local Similarity: 65.22%   Conservative: 0
Query Match: 58.44%   Mismatches: 0
DB: 9   Indels: 40
                                    Gaps: 1

US-10-787-382-10 (1-115) x CB331159 (1-622)

Qy   41 HisGlnLeuCysIleLeuLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAla 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   42 CACCAAACTGTGCATTAAAGAAGAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 101

Qy   61 HisGlyGluAlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGlu   80
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Db   102 CACGGGGAGGCGTGTGGATAAAACTATTCCAAAACTTGTCTTTAATAAAAGAACACATAGAG 161

Qy   81 ArgGln-Lys   83
          |||||| |||
Db   162 CGCCAAAAAGTAAGTTAAAGACATTTGGCAAAAACTTAAGTATATATTTGTCTGACTCTGCC 221

Qy   83 ------   83
Db   222 TGTTTTTTTTTTTTTACAAGAATTGACAGTTTCCTACAATATCTCCTCTGTTCTT 281

Qy   84 ----LysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGl 101
          |||| |||||||||||||||||||||||||||||||||||||||||||||
Db   282 TTAACAGAAAAGGTGGTGCAGAGAAAGATGACAAAAGTTCCTAGACTACCTGCA 341

Qy   101 nValPheLeuGlyValIleAsnThrGluTrpThrProGluSer 115
          ||||||||||||||||||||||||||||||||||||||||
Db   342 AGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 384

ORIGIN

gene   /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    <1..>405
                    /gene="IL5"
                    /locus_tag="HCM4418"

US-10-787-382-10 (1-115) x AY412020 (1-405)

Alignment Scores:

Pred. No.:   1.5e-35
Score: 356.00
Percent Similarity: 76.79%   Matches: 70
Best Local Similarity: 76.79%   Conservative: 16
Query Match: 58.36%   Mismatches: 26
DB: 9   Indels: 0
                                    Gaps: 0

Qy   4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
          ||| ||| || |||| || |||||||||||||||||||||||||||||
Db   67 GAAAATTCCCACCAAGTGCATTGGTGTGAAAGAGAGACCTTGGCACTTTCTACTCATCGAACT 126

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
          ||||||| ||| ||||||||||||||||||||||||||||||||||||||||||
Db   127 CTGCTCGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCACCAAACTG 186

Qy   44 CysIleLysGluValPheGlnGlyIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
          ||: |||:|:||:|||||||||||||||||||||||||||:|:|||||||
Db   187 TGCACTGAAGAAAATCTTTCAGGGAATAGGCACACTGAAGAACCTGAAGGGGT 246

Qy   64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
          |:| :||||||||||||||||||||||||:|:|||:|::|||||||||||
Db   247 ACTGTGGAAAAGACTATTCAAAAACTTGTCTTAATAAAAGAATACATTGACGGCCAAAA 306

Qy   84 LysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
          ||::||||:||||||||||||||||||||||||||:|||||||||||||||||
Db   307 AAAAAGTGGTGCAGAGAAAGATGACAGAGTAAACCAAATTCCTAGACTACCTGCAGAGTTT 366

Qy   104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
          |||||||||||||||||||||||||||||||||||
Db   367 CTTGGGTGTAATAAACACCGAGTGGGATAATAGAAAGT 402

LOCUS   AY412020   405 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY412020
VERSION   AY412020.1 GI:39767985
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 405)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 405)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..405

RESULT 2

RESULT 3

LOCUS   CD559532   456 bp   mRNA   linear   EST 11-JUN-2003
DEFINITION AGENCOURT_14497057 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971772 5', mRNA sequence.
ACCESSION   CD559532
VERSION   CD559532.1 GI:31585600
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 456)
  AUTHORS   Mammalian Gene Collection (MGC)
  TITLE   Direct Submission
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cggebs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK1 row: g column: 11
            High quality sequence stop: 456.
FEATURES   Location/Qualifiers

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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6971772"
                /tissue_type="mixed"
                /lab_host="DH5A (T1 phage-resistant)"
                /clone_lib="NIH_MGC_195"
                /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                loxP-HindIII; Clones from this library have been
                PCR-amplified using gene-specific primers to contain the
                complete open reading frame (based on known gene sequences
                available from NCBI's RefSeq). Template for PCR is cDNA
                derived from either pooled cytoplasmic polyA RNA from 30
                cells lines or pooled total RNA from 10 different tissues
                (from BD Biosciences/Clontech and Washington University).
                PCR products are directionally cloned into the loxP sites
                of the pDNR-Dual vector. Library constructed by Dr.
                Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                Expression Laboratory, Research Technology Program, SAIC
                Frederick, NCI-Frederick, Frederick, MD 21702). For
                information on which gene each clone represents, please
                visit our anonymous ftp site at
                ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                a Note: this is a NIH_MGC Library."

ORIGIN

US-10-787-382-10 (1-115) x CD559532 (1-456)

Alignment Scores:
Pred. No.:              1
Score:                  1.76e-35        Length:        456
Percent Similarity:     356.00          Matches:        70
Best Local Similarity:  76.79%          Conservative:   16
Query Match:            62.50%          Mismatches:     26
DB:                     58.36%          Indels:          0
                        6               Gaps:            0

Qy    4 GluAsnProMetAsnArgLeuValAlaGluThrThrLeuThrLeuLeuSerThrHisArgThr 23
          |||      ::|        ||||||||      ||||||
Db   88 GAAATTCCCACAAGTCGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACATCATCGAACT 147

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHisGlnLeu 43
          ||||||       |||        |||      ||||||
Db  148 CTGCTCGATAGCCAATGAGCACTCTGAGGATTCCGTGTACATAAAAATCACCAACTG 207

Qy   44 CysIleLysGlyValPheGlnHisGlyIleLeuAspThrArgLeuLysAsnGlnThrArgAlaHisGlyGlu 63
          |||     ::::        |||||        ||         |||       ||||
Db  208 TGCACTGAAGAAATCTTTCAGGGAATAGGCACTGGAGAGTCAAACTGTGCAAGGGGT 267

Qy   64 AlaValAspGlyLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
          |||:::||        ||||||||::::||        ||||
Db  268 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAGAAATACATTGACGGCCAAAA 327

Qy   84 LysArgCysAlaGlyGlyArgTrpArgValThrLysPheLeuAspThrTyrLeuGlnValPhe 103
          |||||||:::        ||||||||         |||
Db  328 AAAAAGTGTGGAAGAAGAAGACGGAGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 387

Qy  104 LeuGlyValIleAsnThrGluThrProGluSer 115
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Db  388 CTTGGTGTTAATCAACACCGAGTGGATAATAGAAAGT 423

RESULT 4
LOCUS       CD559686       456 bp    mRNA    linear    EST 11-JUN-2003
DEFINITION  AGENCOURT_14497093 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971772 3', mRNA sequence.
ACCESSION   CD559686
VERSION     CD559686.1  GI:31585754
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1 (bases 1 to 456)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBKi row: g  column: 11
            High quality sequence stop: 456.

FEATURES             Location/Qualifiers
     source          1..456
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971772"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."

ORIGIN

US-10-787-382-10 (1-115) x CD559686 (1-456)

Alignment Scores:
Pred. No.:              1
Score:                  1.76e-35        Length:        456
Percent Similarity:     356.00          Matches:        70
Best Local Similarity:  76.79%          Conservative:   16
Query Match:            62.50%          Mismatches:     26
DB:                     58.36%          Indels:          0
                        6               Gaps:            0

Qy    4 GluAsnProMetAsnArgLeuValAlaGluThrThrLeuThrLeuLeuSerThrHisArgThr 23
          |||      ::|        ||||||||      ||||||
Db  367 GAAATTCCCACAAGTCGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACATCATCGAACT 308

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHisGlnLeu 43
          ||||||       |||        |||      ||||||
Db  307 CTGCTCGATAGCCAATGAGCACTCTGAGGATTCCGTGTACATAAAAATCACCAACTG 248

Qy   44 CysIleLysGlyValPheGlnHisGlyIleLeuAspThrArgLeuLysAsnGlnThrArgAlaHisGlyGlu 63
          |||     ::::        |||||        ||         |||       ||||
Db  247 TGCACTGAAGAAATCTTTCAGGGAATAGGCACTGGAGAGTCAAACTGTGCAAGGGGT 188

Qy   64 AlaValAspGlyLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
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Db  187 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAGAAATACATTGACGGCCAAAA 128

Qy   84 LysArgCysAlaGlyGlyArgTrpArgValThrLysPheLeuAspThrTyrLeuGlnValPhe 103
          |||||||:::        ||||||||         |||
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Db    127 AAAAAGTGTGGAGAAGAAAGACGGGAGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 68
              |||:::|||    |||||||||  ||:||||    ||||  |||||||||||||||||||||||| |||
Qy    104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
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Db     67 CTTGGGTGTAATGAACACCGAGTGGGATAATAGAAAGT 32
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Db:       6         Gaps:      0

US-10-787-382-10 (1-115) x CD559687 (1-470)

Qy      4 GluAsnProMetAsnArgLeuValAlaGluThrHisLeuThrLeuLeuSerThrHisArgThr 23
            |||||||||       :::       |||       :::|||||||||||||||||||||||||||||||||||
Db    320 CTGGCTGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCACCAACTG 261

Qy     24 TrpLeuIleGlyAspTyrAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
            :::|||::|||||||||||:::||||||||||||||||||  |||||  |||||||||||
Db    380 GAAATTCCCACAAGTGCATTGGTGAAAGAGACACCTTGGCACTGCTTTCTTACTCATCGA 321

Qy     44 CysIleGlyGluValPheGlyGlyIleLeuAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
            |||||||  :::|||||||||||||||||||||||||||  |||||||||:::|||||||
Db    260 TGCACTGAAAGAAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGGT 201

Qy     64 AlaValAspLysLeuPheGluAsnLeuSerLeuIleLeuLysGluHisIleIleGluLeuArgGln 83
            |||:::|||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db    200 ACTGTCGAAAAGACTATTCAAAAACTTGTCCTTAATAAAAGAAATACATTGACGGCCAAAA 141

Qy     84 LysArgCysAlaGlyGluValGlyArgTrpArgValThrLysPheLeuAspProTyrLeuGlnValPhe 103
            |||||||:::|||||||||||||||||||||||||||||||||||||||||
Db    140 AAAAAGTGTGGAGAAGACGGAGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 81

Qy    104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
            |||||||||||:::|||||||||||||||||
Db     80 CTTGGGTGTAATGAACACCGAGTGGGATAATAGAAAGT 45
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RESULT 6

CD559533
LOCUS        CD559533                   492 bp    mRNA       linear        EST 26-NOV-2003
DEFINITION   AGENCOURT 14496993 NIH_MGC 195 Homo sapiens cDNA clone
             IMAGE:6971771 5', mRNA sequence.
ACCESSION    CD559533
VERSION      CD559533.2  GI:38558947
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 492)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      On Jun 10, 2003 this sequence version replaced gi:31585601.
             Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics / NIH
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             cDNA Library Preparation: Bhat Laboratory
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: IRBKI  row: g  column: 10
             High quality sequence start: 14
             High quality sequence stop: 492.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971771"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC 195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
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DB:

CD559687/c
LOCUS        CD559687                   470 bp    mRNA       linear        EST 19-NOV-2003
DEFINITION   AGENCOURT 14497029 NIH_MGC 195 Homo sapiens cDNA clone
             IMAGE:6971771 5', mRNA sequence.
ACCESSION    CD559687
VERSION      CD559687.2  GI:38453484
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 470)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      On Jun 10, 2003 this sequence version replaced gi:31585755.
             Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Narayan Bhat
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: IRBKI  row: g  column: 10
             High quality sequence start: 14
             High quality sequence stop: 470.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971771"
                     /tissue_type="mixed"
                     /lab_host="DH5A (T1 phage-resistant)"
                     /clone_lib="NIH_MGC 195"
                     /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
                     loxP-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxP sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN
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Alignment Scores:
Pred. No.:              1.84e-35
Score:                  356.00
Percent Similarity:     76.79%
Best Local Similarity:  62.50%
Query Match:            58.36%

Length:        470
Matches:        70
Conservative:   16
Mismatches:     26
Indels:          0
```

ORIGIN

available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSv.dat
a Note: this is a NIH_MGC Library."

US-10-787-382-10 (1-115) x CD559533 (1-492)

Alignment Scores:
Pred. No.:   1.96e-35
Score: 356.00
Percent Similarity: 76.79%   Length: 492
Best Local Similarity: 62.50%   Matches: 70
Query Match: 58.36%   Conservative: 16
DB: Mismatches: 26
                                        Indels: 0
                                        Gaps: 0

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Qy    4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
          |||    ||||||| |||||||   |||  |  |  |  |    |  |   | |
Db  122 GAAAATTCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCATCGAACT 181

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
          ::  |
Db  182 CTGGCTGGATAGCCAATGAGACTCTGAGGATTCCGTTCCTGTACATAAAAATCACCAACTG 241

Qy   44 CysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
          |||   ||  ||| |||   ||:  |:|  |   |  :|| |
Db  242 TGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGCGAGAGTCAAACTGTGCAAGGGGGT 301

Qy   64 AlaValAspLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
          ||||   |:  |||   ||      ::  ||:       ||::    :
Db  302 ACTGTGGAAGACTATTCAAAAACTTGTCCTTAATAAAGAAAATACATTGACGGCCAAAAA 361

Qy   84 LysArgCysAlaGlyTrpArgTrpProArgValThrLysPheLeuValPhe 103
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Db  362 AAAAAGTGTGGAGAAGAAGACGAGAGGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 421

Qy  104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
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Db  422 CTTGGTGTAATGAACACCGAGTGGGATAATAGAAAGT 457
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RESULT 7
BC066279
LOCUS   BC066279   458 bp   mRNA   linear   HTC 12-FEB-2004
DEFINITION Homo sapiens cDNA clone IMAGE:6971768, containing frame-shift
            errors.
ACCESSION   BC066279
VERSION   BC066279.1 GI:42490901
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 458)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.B.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE   2 (bases 1 to 458)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: a Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 28559032
            This clone has the following problem: frame shifted.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971768"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_195"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-Dual"
ORIGIN

US-10-787-382-10 (1-115) x BC066279 (1-458)

Alignment Scores:
Pred. No.:   8.5e-34
Score: 343.00
Percent Similarity: 76.11%   Length: 458
Best Local Similarity: 61.95%   Matches: 70
Query Match: 56.23%   Conservative: 16
DB: Mismatches: 26
                                        Indels: 1
                                        Gaps: 0

```
Qy    4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
          |||    ||||||| |||||||   |||  |  |  |  |    |  |   | |
Db   90 GAAAATTCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCATCGAACT 149

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
          ::  |
Db  150 CTGGCTGGATAGCCAATGAGACTCTGAGGATTCCGTTCCTGTACATAAAAATCACCAACTG 209

Qy   44 CysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
          |||   ||  ||| |||   ||:  |:|  |   |  :|| |
Db  210 TGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGCGAGAGTCAAACTGTGCAAGGGGGT 269

Qy   64 AlaValAspLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGln-Ly 83
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Db      ...
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Db        270 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAGAATACCATTGACGGCCAAAA 329

Qy         83 SLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPh 103
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Db        330 AAAAAAGTGTGGAGAAGAGACCGGAGGTAAACCAATTCCTAGACTACCTGCAAGAGTT 389

Qy        103 eLeuGlyValIleAsnThrGluTrpThrProGluSer 115
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Db        390 TCTTGGTGTAATGAACACCGGAGTGGATAATAGAAAGT 426
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RESULT 8

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LOCUS       BC066280          458 bp    mRNA        linear   HTC 12-FEB-2004
DEFINITION  Homo sapiens cDNA clone IMAGE:6971769, containing frame-shift
            errors.
ACCESSION   BC066280
VERSION     BC066280.1  GI:4290838
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 458)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanches,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 458)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site:     http://www-shgc.stanford.edu
            Contact:      (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: a Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 28559032
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1..458
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ORIGIN

Alignment Scores:

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Pred. No.:           8.5e-34      Length:              458
Score:               343.00       Matches:             70
Percent Similarity:  76.11%       Conservative:        16
Best Local Similarity: 61.95%     Mismatches:          26
Query Match:         56.23%       Indels:              1
DB:                  3            Gaps:                0
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US-10-787-382-10 (1-115) x BC066280 (1-458)

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Qy          4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuLeuSerThrHisArgThr 23
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Db         90 GAAAATCCCATGAATCGTCATTGGTGAAGAGAGACCTTGGCACTGCTTCTTACTGAACT 149

Qy         24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
              |||:::|            ||||            |||:::|||||||||||
Db        150 CTGCTGATAGCCAATGAACAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCACCA 209

Qy         44 CysIleLysGluValPheGlnGlyIleAspThrArgLeuMetGlnThrArgLeuHisGlyGlu 63
              ||:::|||||||||:::|||:::||||||||||:::|||
Db        210 TGCACTGAAAGAAATTCTTTCAGGGAATAGGCAGACACTGGAGAGTCAAACTGTGCAAGAGGGT 269

Qy         64 AlaValAspLysMetPheGlnAsnLeuSerIleLeuIleGluValArgGln-Ly 83
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Db        270 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAGAATACCATTGACGGCCAAAA 329

Qy         83 SLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPh 103
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Db        330 AAAAAAGTGTGGAGAAGAGACCGGAGGTAAACCAATTCCTAGACTACCTGCAAGAGTT 389

Qy        103 eLeuGlyValIleAsnThrGluTrpThrProGluSer 115
              ||||||||||::|||
Db        390 TCTTGGTGTAATGAACACCGGAGTGGATAATAGAAAGT 426
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RESULT 9

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LOCUS       CD559535                      463 bp    mRNA        linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_14496865 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971769 5', mRNA sequence.
ACCESSION   CD559535
VERSION     CD559535.2  GI:38558950
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 463)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585603.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="PCR rescued clones"
/clone_lib="NIH_MGC_195"
/lab_host="DH10B"
/note="Vector: pDNR-Dual"

Left column

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            PCR-amplified using gene-specific primers to contain the
            complete open reading frame (based on known gene sequences
            available from NCBI's RefSeq). Template for PCR is cDNA
            derived from either pooled cytoplasmic polyA RNA from 30
            cells lines or pooled total RNA from 10 different tissues
            (from BD Biosciences/Clontech and Washington University).
            PCR products are directionally cloned into the loxP sites
            of the pDNR-Dual vector. Library constructed by Dr.
            Narayan Bhat, Earl Bere III and Hongling Liao (Gene
            Expression Laboratory, Research Technology Program, SAIC
            Frederick, NCI-Frederick, Frederick, MD 21702). For
            information on which gene each clone represents, please
            visit our anonymous ftp site at
            ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
            a Note: this is a NIH_MGC Library."

ORIGIN

US-10-787-382-10 (1-115) x CD559535 (1-463)

Alignment Scores:
Pred. No.:
Score:                   8.63e-34        Length:          463
Percent Similarity:      76.11%          Matches:         70
Best Local Similarity:   61.95%          Conservative:    16
Query Match:             56.23%          Mismatches:      26
                                         Indels:          1
                                         Gaps:            0

Qy    4 GluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuSerThrHisArgThr 23
          |||          ||||||||||||||||||||||||||||||||||||
Db  214 TGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAAGAGACTGTCCAAGGGGGT 273

Qy   44 CysIleLeuLysGluValPheGlnGlyIleLeuAspThrLeuLysGlnThrAlaHisGlyGlu 63
          |||     |::::|||||||||||||||||||||||||||||
Db  154 CTGCTGATAGCCAATGAGACTCTGAGGAATTCCGTRCCTGTACATRAAAATCACCAACTG 213

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
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Qy   64 AlaValAspLysArgPheGlnAsnLeuSerLeuIleLeuHisIleGluArgGln-Ly 83
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Db  274 ACTGTGGAAAGACTATTCAAAAACTGTCCTTAATAAAGAAATACATTGACGGCCAAAAA 333

Qy   83 SerLysArgCysAlaGlyValArgValThrLysPheLeuAspThrTyrLeuGlnValPh 103
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Db  334 AAAAAAGTGTGGAGAAGAAAGAACACGAGAGTAAACCAAATTCCTAGACTACCTGCAGAGAGTT 393

Qy  103 eLeuGlyValIleLeuAsnThrGluThrProGluSer 115
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Right column

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RESULT 10
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LOCUS       CD559690       467 bp    mRNA    linear    EST 19-NOV-2003
DEFINITION  AGENCOURT 14496838 NIH_MGC_195 Homo sapiens cDNA clone
            IMAGE:6971768 5', mRNA sequence.
ACCESSION   CD559690
VERSION     CD559690.2  GI:38453490
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 467)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585758.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK1 row: g  column: 07
            High quality sequence stop: 467.

FEATURES    Location/Qualifiers
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            /lab_host="DH5A (T1 phage-resistant)"
            /clone_lib="NIH_MGC_195"
            /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
            loxP-HindIII; Clones from this library have been
            PCR-amplified using gene-specific primers to contain the
            complete open reading frame (based on known gene sequences
            available from NCBI's RefSeq). Template for PCR is cDNA
            derived from either pooled cytoplasmic polyA RNA from 30
            cells lines or pooled total RNA from 10 different tissues
            (from BD Biosciences/Clontech and Washington University).
            PCR products are directionally cloned into the loxP sites
            of the pDNR-Dual vector. Library constructed by Dr.
            Narayan Bhat, Earl Bere III and Hongling Liao (Gene
            Expression Laboratory, Research Technology Program, SAIC
            Frederick, NCI-Frederick, Frederick, MD 21702). For
            information on which gene each clone represents, please
            visit our anonymous ftp site at
            ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
            a Note: this is a NIH_MGC Library."

ORIGIN

US-10-787-382-10 (1-115) x CD559690 (1-467)

Alignment Scores:
Pred. No.:
Score:                   8.73e-34        Length:          467
Percent Similarity:      76.11%          Matches:         70
Best Local Similarity:   61.95%          Conservative:    16
Query Match:             56.23%          Mismatches:      26
                                         Indels:          1
                                         Gaps:            0

Qy    4 GluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuSerThrHisArgThr 23
          :::                |||||   |||   ||||||
Db  377 GAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTACTCATCGAACT 318

Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
          |||     |::::|||||||||||||||||||||||||||||
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Qy   44 CysIleLeuLysGluValPheGlnGlyIleLeuAspThrLeuLysGlnThrAlaHisGlyGlu 63
          |||          ||||||||||||||||||||||||||||||||||||
Db  257 TGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAAGAGACTGTCCAAGGGGGT 198

Qy   64 AlaValAspLysArgPheGlnAsnLeuSerLeuIleLeuHisIleGluArgGln-Ly 83
          ||||::::||||||||::::||||||||:::      |||
Db   64 ...
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RESULT 11

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Qy   197 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAAGAAAATACATTGACGGCCAAAA 138
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Qy   103 eLeuGlyValIleAsnThrGluTrpThrProThrProGluSer 115
         |||::||||||||||||::||::|||||||||||||||||||
Db    77 TCTTGGTGTAATGAACACCCGAGTGGATAATAGAAAGT 41
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Score: 343.00   Matches: 70
Percent Similarity: 76.11%   Conservative: 16
Best Local Similarity: 61.95%   Mismatches: 26
Query Match: 56.23%   Indels: 1
DB: 6   Gaps: 0
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RESULT 12

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Qy     4 GluAsnProMetAsnArgLeuValAlaGluThrThrLeuThrLeuLeuSerThrHisArgThr 23
         |||||||  :::|||           |||||  ||||||::|||::|||||||::|||
Db   383 GAAATTCCCACAAGTGCATTGGTGAAAGAGACCTTGGCACTGCTTTCTTACCTCATCGAACT 324

Qy    24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
         ||||||              |||||||||||||||||  |||||||||||||||||
Db   323 CTGCTGATAGCCAATGAGACTCTGAGGAATTCCTGTTCCGTGACATAAAAAATCACACTG 264

Qy    44 CysIleGlyLysGluValPheGluGlnGlyIleIleAspThrLeuLysAsnGlnThrArgLeuHisGlyGlu 63
         ||:||  |||||||::|||||||||:  :|||||||||||||||::||::|||||||||
Db   263 TGCACTGCGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAAACTGTGCAAGGGGT 204

Qy    64 AlaValAspGlysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleIleGluGluArgGln-Lys 83
         |||:|||||||||||||||||||::|::|||||||||||||||||||||||||::||
Db   203 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAAGAAAATACATTGACGGCCAAAA 144

Qy    83 sLysArgCysAlaGlyGluArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPh 103
         ||||||||||||||:|||:||||||||||:||||::|||||||||||||||  |||
Db   143 AAAAAAGTGTGGAGAAGAACGGAGAGGTAAACCAATTCCTAGACTACCTGCAAGAGTT 84

Qy   103 eLeuGlyValIleAsnThrGluTrpThrProThrProGluSer 115
         |||::||||||||||||::||::|||||||||||||||||||
Db    83 TCTTGGTGTAATGAACACCCGAGTGGATAATAGAAAGT 47
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```

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ORIGIN

/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat a Note: this is a NIH_MGC Library."

Alignment Scores:
Pred. No.:
Score:                  9.29e-34          Length:         489
                        343.00            Matches:        70
Percent Similarity:     76.11%            Conservative:   16
Best Local Similarity:  61.95%            Mismatches:     26
Query Match:            56.23%            Indels:         1
DB:                     6                 Gaps:           0

US-10-787-382-10 (1-115) x CD559536 (1-489)

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Qy   4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArgThr 23
       ||| ||| ::
Db 120 GAAAATCCACAAGTGCATTGGTGAAAGAGACCTGGCACTGCTTTCTACTCATCGAACT 179

Qy 24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
       ||||||||||||||| :::|::::
Db 180 CTGCTGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCACCAACTG 239

Qy 44 CysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
       ||||||||| ::::|||||||
Db 240 TGCACTGAAGAGAAATCTTTCAGGGAATAGGCACACTGCTCAAACTGTGCCAAGGGGGT 299

Qy 64 AlaValAspLysValLeuPheGlnAsnLeuSerLeuIleLysGluGluHisIleGluArgGln-Ly 83
       ||||||||||| :::::|:::||:::
Db 300 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAGAATACAATTGACGGCCAAAA 359

Qy 83 GlysArgCysAlaGlyGlyLeuArgTrpArgValThrLysPheLeuAspThrTyrLeuGlnValPh 103
       ||| || |:||
Db 360 AAAAAAGTGTGGAGAGAGGAGAGGAGTAAACCAATTCCTAGACTACCCTGCAAGAGTT 419

Qy 103 eLeuGlyValIleLeuAsnThrGluThrTrpThrProGluSer 115
       |||||||||| ||||
Db 420 TCTTGGTGTAATGAACACCGAGTGGATAATAGAAGT 456
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Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE   Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED   12477932
REFERENCE   2 (bases 1 to 817)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Anup Madan, University of Iowa
            cDNA Library Preparation: Anup Madan, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Neurogenomics Research Lab,
            200 B EMRB, University of Iowa, Iowa City, IA-52242
            anup-madan@uiowa.edu
            Jessica Fahey, Tim Nelson, Jae Goon Yoon and Anup Madan
            This clone has the following problem: frame shifted.
            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: Plate: Row: Column: 0

FEATURES   Location/Qualifiers
     source   1..817
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7216996"
                     /tissue_type="Synthetic constructs"
                     /clone_lib="NIH_MGC_243"
                     /lab_host="TOP10"
                     /note="Vector: pCR Blunt II TOPO"

ORIGIN

US-10-787-382-10 (1-115) x BC069137 (1-817)

Alignment Scores:
Pred. No.:
Score: 1.87e-33   Length: 817
                        343.00   Matches: 70
Percent Similarity: 76.11%   Conservative: 16
Best Local Similarity: 61.95%   Mismatches: 26
Query Match: 56.23%   Indels: 1
DB: 3   Gaps: 0

```
Qy   4 GluAsnProMetAsnArgLeuValAlaGluThrLeuThrLeuSerThrHisArgThr 23
       |||     :::
Db 111 GAAATTCCACAAGTGCATTGGTGAAAGAGACCTGGCACTGCTTTCTACTCATCGAACT 170

Qy  24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
       ||||||||||||||     ::::
Db 171 CTGCTGATAGCCAATGAGACTCTGAGGATTCCTGTTCCTGTACATAAAAATCACCAACTG 230

Qy  44 CysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
       |||   ::||||||||
Db 231 TGCACTGAAGAGAAATCTTTCAGGGAATAGGCACACTGCTCAAACTGTGCCAAGGGGGT 290

Qy  64 AlaValAspLysValLeuPheGlnAsnLeuSerLeuIleLysGluGluHisIleGluArgGln-Ly 83
       |||     :::::     |||   ||
Db ... 
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RESULT 13
LOCUS   BC069137   817 bp   mRNA   linear   HTC   26-APR-2004
DEFINITION Homo sapiens cDNA clone IMAGE:7216996, containing frame-shift errors.
ACCESSION   BC069137
VERSION   BC069137.1 GI:46575644
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 817)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

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Db  291 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGACGGCCAAAAA 350
Qy   83 sLysArgCysAlaGlyGlyLeuArgTrpArgValThrLysPheLeuAspThrLeuGlnValPh 103
        |||::::|||:|
Db  351 GAAAAAGTGTGGAGAAGAAGAAGAGAGTAAACCAATTCCTAGACTACCTGCAAGAGTT 410
Qy  103 eLeuGlyValIleAsnThrGluTrpThrProGluSer 115
        ||:::||::||||||||||
Db  411 TCTTGGTGTAATGAACACCGGAGTGGATAATAGAAAGT 447
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RESULT 14
LOCUS   AY412021   405 bp   DNA   linear   GSS 16-DEC-2003
DEFINITION Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY412021
VERSION   AY412021.1 GI:39767986
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 405)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 405)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
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                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1..>405
                     /gene="IL5"
                     /locus_tag="HCM4418"
ORIGIN

US-10-787-382-10 (1-115) x AY412021 (1-405)

Alignment Scores:
Pred. No.:   4.28e-33
Score: 337.00   Length: 405
Percent Similarity: 74.11%   Matches: 68
Best Local Similarity: 60.71%   Conservative: 15
Query Match: 55.25%   Mismatches: 29
DB: 9   Indels: 0
                                        Gaps: 0
```

```
Qy    4 GluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuSerThrHisArgThr  23
          ||||:::|||:|||:|||||||::|         ||||||||||:||||
Db    4 GAAATTCCACAAGTGCATGGTGAAAAGACCCTGGCACTGCTTTCTACTCATCGAACT 126
Qy   24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLeuAsnHisGlnLeu 43
          |||:::||||:|||||
Db  127 CTGCTAATAGGCCAATGAGACTCTGAGGAATTCCTGTTCCTGTACATAAAAATCACCAACNN 186
Qy   44 CysIleLysGluValPheGlnGlyIleLeuAspThrLeuAsnGlnThrLeuAlaHisGlyGlu 63
          ::::|||||||||||||||||:::||||||||::|||:|
Db  187 NGCACTGAGAGAAATCTTTCAGGGAATAGGCACACTGTGCACAGGGGGT 246
```

```
Qy   64 AlaValAlaAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
          |||::::|||:|||:|||||||::|
Db  247 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAGAAATACATTGACGGCCAAAAA 306
Qy   84 LysArgCysAlaGlyGlyLeuArgTrpArgValThrLysPheLeuAspThrLeuGlnValPhe 103
          |||:::|||:||||:||||||||
Db  307 AAAAAGTGTGGAGAAGAAGAAGAGAGTAAACCAATTCCTAGACTACCTGCAAGAGTT 366
Qy  104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
          ||::::||::||||||||
Db  367 CTTGGTGTAATGAACACCGGAGTGGATAATAGAAAGT 402
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RESULT 15
LOCUS   BC066281   456 bp   mRNA   linear   HTC 12-FEB-2004
DEFINITION Homo sapiens cDNA clone IMAGE:6971770, containing frame-shift
            errors.
ACCESSION   BC066281
VERSION   BC066281.1 GI:42469969
KEYWORDS   HTC.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 456)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED   12477932
REFERENCE   2 (bases 1 to 456)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (03-FEB-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 172 Row: a Column: 17
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 28559032
            This clone has the following problem: frame shifted.

FEATURES
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　　　　　　　/tissue_type="PCR rescued clones"
　　　　　　　/clone_lib="NIH_MGC_195"
　　　　　　　/lab_host="DH10B"
　　　　　　　/note="Vector: pDNR-Dual"

ORIGIN

Alignment Scores:
Pred. No.:　　　　　　　　　1
Score:　　　　　　　　　2.23e-32　　Length:　　　　456
Percent Similarity:　　332.00　　Matches:　　　　70
Best Local Similarity: 75.89%　　Conservative:　15
Query Match:　　　　62.50%　　Mismatches:　　27
DB:　　　　　　　　54.43%　　Indels:　　　　1
　　　　　　　　　　3　　　　Gaps:　　　　　0

US-10-787-382-10 (1-115) x BC066281 (1-456)

Qy　　4 GluAsnProMetAsnArgLeuValAlaGlyThrLeuThrLeuSerThrHisArgThr 23
　　　　|||　　|||||||||||||||||||||||||||||||||||||||||||||||
Db　90 GAAATTCCCACAAGTGCATTGGGTGAAAGAGACCTTGGCACTTCTTCATCATCGAACT 149

Qy　24 TrpLeuIleGlyAspGlyAsnLeuMetIleProThrProGluAsnLysAsnHisGlnLeu 43
　　　　||||||　　　　：：：||||||　　|||　|||||||：：||||||||
Db　150 CTGCTGATAGCCAATGAGACTCTGAGGACTTCCTGTTCCTGTACATAAAAATCACCAAACTG 209

Qy　44 CysIleLysGluValPheGlnGlyIleIleAspThrLeuLysAsnGlnThrAlaHisGlyGlu 63
　　　　||||||：|||||||：：||||||||||||：：：：：||||||||：||||||||
Db　210 TGCACTGAAGAAAATCTTTCAGGGAATAAGGCACACTGGAGAGTCAAACTGTGCAAGGGGGT 269

Qy　64 AlaValAspLysLeuPheGlnAsnLeuSerLeuIleLysGluHisIleGluArgGlnLys 83
　　　　||||：：：：：||||：：||||||||||||||：：：：||||　　||||||||
Db　270 ACTGTGGAAAGACTATTCAAAAACTTGTCCTTAATAAAAGAAATACATTGA-CGGCCAAAA 328

Qy　84 LysArgCysAlaGlyGlyArgTrpArgValThrLysPheLeuAspTyrLeuGlnValPhe 103
　　　　||||：：|||　　||||||||||||||||||||：：：||||||||||||||||
Db　329 AAAAAGTGTGGAGAGAAAGACGGAGGAGTAAACCAATTCCTAGACTACCTGCAAGAGTTT 388

Qy　104 LeuGlyValIleAsnThrGluTrpThrProGluSer 115
　　　　|||||||||||：：：||||||||||||||||||
Db　389 CTTGGTGTAATGAACACCGAGTGGGATAATAGAAAGT 424

Search completed: August 7, 2005, 00:10:30
Job time : 2418 secs